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=> file biosis caba caplus embase japio lifesci medline scisearch
=> e kim bum joon/au
E1      48      KIM BUM JIN/AU
E2      1      KIM BUM JO/AU
E3      358    --> KIM BUM JOON/AU
E4      3      KIM BUM JOON DR/AU
E5      1      KIM BUM JOON DR PROF/AU
E6      43     KIM BUM JUN/AU
E7      1      KIM BUM JUNE/AU
E8      1      KIM BUM KEE/AU
E9      8      KIM BUM KEUN/AU
E10     5      KIM BUM KI/AU
E11     2      KIM BUM KWAN/AU
E12     4      KIM BUM KWON/AU
=> s e2-e7 and hsp?
L1      49     ("KIM BUM JO"/AU OR "KIM BUM JOON"/AU OR "KIM BUM JOON DR"/AU
           OR "KIM BUM JOON DR PROF"/AU OR "KIM BUM JUN"/AU OR "KIM BUM
           JUNE"/AU) AND HSP?

=> dup rem l1
PROCESSING COMPLETED FOR L1
L2      15     DUP REM L1 (34 DUPLICATES REMOVED)
=> d bib ab kwic l-
YOU HAVE REQUESTED DATA FROM 15 ANSWERS - CONTINUE? Y/(N):y

L2      ANSWER 1 OF 15      MEDLINE on STN
AN      2009107816      MEDLINE <<LOGINID::20090617>>
DN      PubMed ID: 19041640
TI      Chicken Ovalbumin Upstream Promoter-Transcription Factor II (COUP-TFII)
           regulates growth and patterning of the postnatal mouse cerebellum.
AU      ***Kim Bum Jun*** ; Takamoto Norio; Yan Jun; Tsai Sophia Y; Tsai
           Ming-Jer
CS      Department of Molecular and Cellular Biology and Development Program,
           Baylor College of Medicine, Houston, TX 77030, USA.
NC      DK45641 (United States NIDDK NIH HHS)
           HD17379 (United States NICHD NIH HHS)
           HL076448 (United States NHLBI NIH HHS)
           P01 DK059820-060003 (United States NIDDK NIH HHS)
           P01 DK059820-070003 (United States NIDDK NIH HHS)
           P01 DK059820-080003 (United States NIDDK NIH HHS)
           P01DK59820 (United States NIDDK NIH HHS)
           R01 HD017379-22A1 (United States NICHD NIH HHS)
           R01 HD017379-23 (United States NICHD NIH HHS)
           R01 HD017379-24 (United States NICHD NIH HHS)
           R01 HL076448-02 (United States NHLBI NIH HHS)
           R01 HL076448-03 (United States NHLBI NIH HHS)
           R01 HL076448-04 (United States NHLBI NIH HHS)
           R37 DK045641-13 (United States NIDDK NIH HHS)
           R37 DK045641-14 (United States NIDDK NIH HHS)
           R37 DK045641-15 (United States NIDDK NIH HHS)
           R37 DK045641-16 (United States NIDDK NIH HHS)
           R37 DK045641-17 (United States NIDDK NIH HHS)
           U19 DK062434-010006 (United States NIDDK NIH HHS)
           U19 DK062434-01S10006 (United States NIDDK NIH HHS)
           U19 DK062434-01S19003 (United States NIDDK NIH HHS)
SO      Developmental biology, (2009 Feb 15) Vol. 326, No. 2, pp. 378-91.
           Electronic Publication: 2008-11-14.

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Journal code: 0372762. E-ISSN: 1095-564X.
 Report No.: NLM-NIHMS94374; NLM-PMC2654226.

CY United States
 DT Journal; Article; (JOURNAL ARTICLE)
 (RESEARCH SUPPORT, N.I.H., EXTRAMURAL)
 LA English
 FS Priority Journals
 EM 200902
 ED Entered STN: 3 Feb 2009
 Last Updated on STN: 26 Feb 2009
 Entered Medline: 25 Feb 2009

AB COUP-TFII (also known as Nr2f2), a member of the nuclear orphan receptor superfamily, is expressed in several regions of the central nervous system (CNS), including the ventral thalamus, hypothalamus, midbrain, pons, and spinal cord. To address the function of COUP-TFII in the CNS, we generated conditional COUP-TFII knockout mice using a tissue-specific NSE-Cre recombinase. Ablation of COUP-TFII in the brain resulted in malformation of the lobule VI in the cerebellum and a decrease in differentiation of cerebellar neurons and cerebellar growth. The decrease in cerebellar growth in NSE(Cre+)/CII(F/F) mice is due to reduced proliferation and increased apoptosis in granule cell precursors (GCPs). Additional studies demonstrated that insulin like growth factor 1 (IGF-1) expression was reduced in the cerebellum of NSE(Cre+)/CII(F/F) mice, thereby leading to decreased Akt1 and GSK-3beta activities, and the reduced expression of mTOR. Using ChIP assays, we demonstrated that COUP-TFII was recruited to the promoter region of IGF-1 in a Spl-dependent manner. In addition, dendritic branching of Purkinje cells was decreased in the mutant mice. Thus, our results indicate that COUP-TFII regulates growth and maturation of the mouse postnatal cerebellum through modulation of IGF-1 expression.

AU ***Kim Bum Jun*** ; Takamoto Norio; Yan Jun; Tsai Sophia Y; Tsai Ming-Jer

CT . . . Proliferation
 *Cerebellum: AH, anatomy & histology
 *Cerebellum: GD, growth & development
 Cerebellum: ME, metabolism
 Glycogen Synthase Kinase 3: ME, metabolism
 *** HSP70 Heat-Shock Proteins: ME, metabolism***
 Humans
 Insulin-Like Growth Factor I: GE, genetics
 Insulin-Like Growth Factor I: ME, metabolism
 Mice
 Mice, . . .

CN 0 (COUP Transcription Factor II); 0 (Calcium-Binding Protein, Vitamin D-Dependent); 0 (Carrier Proteins); 0 (***HSP70*** Heat-Shock Proteins); 0 (RNA, Small Interfering); 0 (calbindin); 0 (calretinin); EC 2.7.1 (Frap1 protein, mouse); EC 2.7.1.- (Phosphotransferases (Alcohol Group. . .

L2 ANSWER 2 OF 15 CAPLUS COPYRIGHT 2009 ACS on STN DUPLICATE 1
 AN 2008:1298911 CAPLUS <LOGINID::20090617>>
 TI Proportions of Mycobacterium massiliense and Mycobacterium bolletii strains among Korean Mycobacterium chelonae-Mycobacterium abscessus group isolates

AU Kim, Hee-Young; Kook, Yoonwon; Yun, Yeo-Jun; Park, Chan Geun; Lee, Nam Yong; Shim, Tae Sun; ***Kim, Bum-Joon*** ; Kook, Yoon-Hoh
 CS Department of Microbiology, Cancer Research Institute, Institute of

Endemic Diseases, SNUMRC, and Clinical Research Institute, Seoul National University College of Medicine, Seoul National University Hospital, Seoul, 110-799, S. Korea

SO Journal of Clinical Microbiology (2008), 46(10), 3384-3390
CODEN: JCMIDW; ISSN: 0095-1137

PB American Society for Microbiology
DT Journal
LA English

AB Korean isolates of the *Mycobacterium chelonae*-*Mycobacterium abscessus* group, which had been isolated from two different hospitals in South Korea, were identified by PCR restriction anal. (PRA) and comparative sequence anal. of 16S rRNA genes, *rpoB*, and ***hsp65*** to evaluate the proportion of four closely related species (*M. chelonae*, *M. abscessus*, *M. massiliense*, and *M. bolletii*). Of the 144 rapidly growing mycobacterial strains tested, 127 strains (88.2%) belonged to the *M. chelonae*-*M. abscessus* group. In this group, *M. chelonae*, *M. abscessus*, *M. massiliense*, and *M. bolletii* accounted for 0.8% (n = 1), 51.2% (n = 65), 46.5% (n = 59), and 1.6% (n = 2), resp. Two isolates which showed discordant results, *M. massiliense* by *rpoB* sequence anal. and *M. abscessus* by ***hsp65*** sequence anal., were finally identified as *M. massiliense* based on the addnl. anal. of *sodA* and the 16S-23S internal transcribed spacer. *M. abscessus* group I isolates previously identified by ***hsp65*** PRA were all found to be *M. abscessus*, whereas group II isolates were further identified as *M. massiliense* or *M. bolletii* by sequencing of *rpoB* and ***hsp65***. Smooth, rough, or mixed colonies of both *M. abscessus* and *M. massiliense* isolates were obsd. *M. massiliense* strains that were highly resistant to clarithromycin had a point mutation at the adenine at position 2058 (A2058) or 2059 (A2059) in the peptidyltransferase region of the 23S rRNA gene.

RE.CNT 42 THERE ARE 42 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

AU Kim, Hee-Youn; Kook, Yoonwon; Yun, Yeo-Jun; Park, Chan Geun; Lee, Nam Yong; Shim, Tae Sun; ***Kim, Bum-Joon*** ; Kook, Yoon-Hoh

AB . . . in South Korea, were identified by PCR restriction anal. (PRA) and comparative sequence anal. of 16S rRNA genes, *rpoB*, and ***hsp65*** to evaluate the proportion of four closely related species (*M. chelonae*, *M. abscessus*, *M. massiliense*, and *M. bolletii*). Of the . . . (n = 2), resp. Two isolates which showed discordant results, *M. massiliense* by *rpoB* sequence anal. and *M. abscessus* by ***hsp65*** sequence anal., were finally identified as *M. massiliense* based on the addnl. anal. of *sodA* and the 16S-23S internal transcribed spacer. *M. abscessus* group I isolates previously identified by ***hsp65*** PRA were all found to be *M. abscessus*, whereas group II isolates were further identified as *M. massiliense* or *M. bolletii* by sequencing of *rpoB* and ***hsp65***. Smooth, rough, or mixed colonies of both *M. abscessus* and *M. massiliense* isolates were obsd. *M. massiliense* strains that were. . .

ST Mycobacterium ***hsp65*** *rpoB* 16S rRNA gene
IT INDEXING IN PROGRESS
IT INDEXING IN PROGRESS
IT Human
Mycobacterium abscessus
Mycobacterium bolletii
Mycobacterium chelonae
Mycobacterium massiliense
(*M. chelonae*-*M. abscessus* group isolate from Korean patient show high prevalence of *M. massiliense*, *M. abscessus* and *M. massiliense*, *M. bolletii* accounted for *M. abscessus* group II strains identified by

hsp65 PCR restriction anal.)

L2 ANSWER 3 OF 15 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN
DUPLICATE 2
AN 2008:322988 BIOSIS <<LOGINID::20090617>>
DN PREV200800322987
TI *Mycobacterium sensu* sp nov., a slowly growing, non-chromogenic species
closely related to the *Mycobacterium terrae* complex.
AU Mun, Ho-Suk; Park, Joo-Hee; Kim, Hong; Yu, Hee-Kyung; Park, Young-Gil;
Cha, Chang-Yong; Kook, Yoon-Hoh; ***Kim, Bum-Joon*** [Reprint Author]
CS Seoul Natl Univ, Coll Med, Dept Microbiol and Immunol, Canc Res Inst,
Seoul 110799, South Korea
kbumjoon@snu.ac.kr
SO International Journal of Systematic and Evolutionary Microbiology, (MAR
2008) Vol. 58, No. Part 3, pp. 641-646.
ISSN: 1466-5026.
DT Article
LA English
OS GenBank-DQ536407; EMBL-DQ536407; DDJB-DQ536407; GenBank-DQ536409;
EMBL-DQ536409; DDJB-DQ536409
ED Entered STN: 29 May 2008
Last Updated on STN: 29 May 2008
AB A previously undescribed, slowly growing, non-chromogenic mycobacterium,
isolated from a Korean patient with a symptomatic pulmonary infection, is
described as representing a novel species. Its 16S rRNA gene sequence was
unique and phylogenetic analysis based on 16S rRNA gene sequences showed
that this organism belonged to the *Mycobacterium terrae* subclade.
Phenotypically, the strain was generally similar to *M. terrae* and
Mycobacterium nonchromogenicum, but its growth rate was slower than those
of other *M. terrae* complex strains. A unique mycolic acid profile and
phylogenetic analysis based on two different alternative chronometer
molecules, ***hsp65*** and *rpoB*, confirm the taxonomic status of this
strain as a representative of a novel species. The name *Mycobacterium*
sensu sp. nov. is proposed, with the type strain 05-832(T) (=DSM
44999(T) =KCTC 19147(T)).
AU Mun, Ho-Suk; Park, Joo-Hee; Kim, Hong; Yu, Hee-Kyung; Park, Young-Gil;
Cha, Chang-Yong; Kook, Yoon-Hoh; ***Kim, Bum-Joon*** [Reprint Author]
AB. . . other *M. terrae* complex strains. A unique mycolic acid profile and
phylogenetic analysis based on two different alternative chronometer
molecules, ***hsp65*** and *rpoB*, confirm the taxonomic status of this
strain as a representative of a novel species. The name *Mycobacterium*
sensu sp. nov. is proposed, with the type strain 05-832(T) (=DSM
44999(T) =KCTC 19147(T)).
IT Major Concepts
Population Genetics (Population Studies); Systematics and Taxonomy
IT Chemicals & Biochemicals
rpoB; ***hsp65*** ; 16S ribosomal RNA [16S rRNA, gene sequence]
L2 ANSWER 4 OF 15 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN
DUPLICATE 3
AN 2008:636733 BIOSIS <<LOGINID::20090617>>
DN PREV200800636732
TI Differentiation of mycobacteria in sputa by duplex polymerase chain
reaction for mycobacterial ***hsp65*** gene.
AU ***Kim, Bum-Joon*** [Reprint Author]; Park, Joo-Hee; Lee, Seoung-Ae;
Kim, Hong; Cha, Chang-Yong; Kook, Yoon-Hoh; Kim, Eui-Chong; Joo, Sei Ick;
Lee, Jae Seok; Yim, Jae-Joon
CS Seoul Natl Univ, Coll Med, Canc Res Inst, Dept Microbiol and Immunol,

Seoul 110744, South Korea
 kbumjoon@snu.ac.kr; yimjj@snu.ac.kr

SO Diagnostic Microbiology and Infectious Disease, (OCT 2008) Vol. 62, No. 2,
 pp. 193-198.
 CODEN: DMIDDZ. ISSN: 0732-8893.

DT Article
 LA English
 ED Entered STN: 19 Nov 2008
 Last Updated on STN: 19 Nov 2008

AB Early differentiation of mycobacteria in Sputa is crucial. This study was
 set to evaluate the usefulness of a newly developed duplex polymerase
 chain reaction (PCR) for ***hsp65*** gene-based method in
 differentiating mycobacteria in sputum with a positive acid-fast bacilli
 (AFB) smear before culturing. One hundred forty-seven sputa with positive
 AFB smear were included for the analysis. Mycobacterial species
 identified using a newly developed duplex PCR for ***hsp65*** gene
 followed by a nested PCR-direct were sequencing and the conventional
 colony-based method. Final decision of mycobacterial species were made
 based on 1) results of species identification based on mycobacterial
 colonies or 2) results of species identification of other sputa from the
 same patients and clinical findings. The duplex PCR-based method
 correctly identified 83.2% Sputa from tuberculosis patients and 82.2%
 sputa from nontuberculous mycobacteria patients, whereas the colony-based
 method correctly identified 86.1% and 77.8%, respectively. Sensitivity
 and specificity of the colony-based method for Mycobacterium tuberculosis
 were 86.1% and 100%, respectively, whereas those of the duplex PCR-based
 method were 83.2% and 95.6%, respectively. The duplex PCR-based method,
 to differentiate mycobacterial species in Sputa, produced comparable
 results as those of the colony-based identification method. (C) 2008
 Elsevier Inc. All rights reserved.

TI Differentiation of mycobacteria in sputa by duplex polymerase chain
 reaction for mycobacterial ***hsp65*** gene.

AU ***Kim, Bum-Joon*** [Reprint Author]; Park, Joo-Hee; Lee, Seoung-Ae;
 Kim, Hong; Cha, Chang-Yong; Kook, Yoon-Hoh; Kim, Eui-Chong; Joo, Sei Ick;
 Lee, Jae. . .

AB. . . is crucial. This study was set to evaluate the usefulness of a
 newly developed duplex polymerase chain reaction (PCR) for ***hsp65***
 gene-based method in differentiating mycobacteria in sputum with a
 positive acid-fast bacilli (AFB) smear before culturing. One hundred
 forty-seven sputa with positive AFB smear were included for the analysis.
 Mycobacterial species identified using a newly developed duplex PCR for
 hsp65 gene followed by a nested PCR-direct were sequencing and
 the conventional colony-based method. Final decision of mycobacterial species
 were made. . .

GEN Mycobacterium ***hsp65*** gene (Mycobacteriaceae)

L2 ANSWER 5 OF 15 CAPLUS COPYRIGHT 2009 ACS on STN
 AN 2007:1057364 CAPLUS <<LOGINID::20090617>>
 DN 147:337125

TI Method for differentiating or identifying Mycobacterium tuberculosis and
 non-tuberculous mycobacteria using ***hsp65*** signature nucleotide
 sequence

IN ***Kim, Bum Joon*** ; Kim, Hyun Joo; Park, Hae Joon
 PA Seoul National University Industry Foundation, S. Korea
 SO Repub. Korea, No pp. given
 CODEN: KRXXFC

DT Patent
LA Korean
FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	KR 692484	B1	20070313	KR 2005-104871	20051103
PRAI	KR 2005-104871		20051103		

AB A method for identifying Mycobacterium tuberculosis and non-tuberculous mycobacteria is provided to conveniently and accurately differentiate Mycobacterial species by using each 8 signature nucleotide sequences capable of characterizing Mycobacterium tuberculosis group and non-tuberculous mycobacteria group. The method comprises the steps of: (a) amplifying a gene fragment including at least one base selected from the group consisting of bases located at 228th, 243th, 543th, 600th, 705th, and 718-720th from a 5'-terminal of a heat shock protein 65(***HSP65***) consisting of total 1623bp of Mycobacterial species using

a primer specifically amplifying thereof; (b) analyzing the nucleotide sequence of the amplified gene fragment; and (c) comparing the bases above to identify non-tuberculous mycobacteria and Mycobacterium tuberculosis, where the non-tuberculous mycobacteria is 228th base of C, 243th base of C, 543th base of C, 600th base of C or T, 705th base of G or 718-720th bases of CAG, and the Mycobacterium tuberculosis is 228th base of A, 243th base of T, 543th base of T, 600th base of G, 705th base of C or 718-720th bases of GGA. The nucleotide sequence of primer pair for producing PCR amplification product specific to the non-tuberculous mycobacteria is described. The differentiation kit for non-tuberculous mycobacteria and Mycobacterium tuberculosis comprises a primer pairs, and the sequences of the primers have been presented.

TI Method for differentiating or identifying Mycobacterium tuberculosis and non-tuberculous mycobacteria using ***hsp65*** signature nucleotide sequence

IN ***Kim, Bum Joon*** ; Kim, Hyun Joo; Park, Hae Joon
AB . . . consisting of bases located at 228th, 243th, 543th, 600th, 705th, and 718-720th from a 5'-terminal of a heat shock protein 65(***HSP65***) consisting of total 1623bp of Mycobacterial species using a primer specifically amplifying thereof; (b) analyzing the nucleotide sequence of the. . .

ST Mycobacterium tuberculosis nontuberculous genotyping PCR ***Hsp65*** gene

IT Heat-shock proteins
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(***HSP*** 65; method for differentiating or identifying Mycobacterium tuberculosis and non-tuberculous mycobacteria using ***hsp65*** signature nucleotide sequence)

IT Gene, microbial
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(***hsp65*** ; method for differentiating or identifying Mycobacterium tuberculosis and non-tuberculous mycobacteria using ***hsp65*** signature nucleotide sequence)

II Genotypes
Genotyping (method)
Mycobacterium
Mycobacterium tuberculosis
Polymerase chain reaction
Tuberculosis
(method for differentiating or identifying Mycobacterium tuberculosis

and non-tuberculous mycobacteria using ***hsp65*** signature
nucleotide sequence)

IT Primers (nucleic acid)
RL: ARG (Analytical reagent use); BSU (Biological study, unclassified);
ANST (Analytical study); BIOL (Biological study); USES (Uses)
(method for differentiating or identifying Mycobacterium tuberculosis
and non-tuberculous mycobacteria using ***hsp65*** signature
nucleotide sequence)

L2 ANSWER 6 OF 15 SCISEARCH COPYRIGHT (c) 2009 The Thomson Corporation on
STN

AN 2007:1225201 SCISEARCH <<LOGINID::20090617>>

GA The Genuine Article (R) Number: 231FU

TI Case of pyomyositis due to Mycobacterium haemophilum in a renal transplant
recipient

AU Choi, Sang-Ho (Reprint)

CS Univ Ulsan, Coll Med, Asan Med Ctr, Div Infect Dis, Seoul 138736, South
Korea (Reprint)

AU Jang, Eun-Young; Lee, Sang-Oh; Choi, Seong-Ho; Sung, Heungsup; Kim, Mi-Na;
Kim, Bum-Joon ; Kim, Yang Soo; Woo, Jun Hee

CS Univ Ulsan, Coll Med, Asan Med Ctr, Dept Lab Med, Seoul 138736, South
Korea; Seoul Natl Univ, Coll Med, Liver Res Inst, Canc Res Inst, Dept
Microbiol & Immunol, Seoul, South Korea
E-mail: sangho@amc.seoul.kr

CYA South Korea

SO JOURNAL OF CLINICAL MICROBIOLOGY, (NOV 2007) Vol. 45, No. 11, pp.
3847-3849.
ISSN: 0095-1137.

PB AMER SOC MICROBIOLOGY, 1752 N ST NW, WASHINGTON, DC 20036-2904 USA.

DT Article; Journal

LA English

REC Reference Count: 13

ED Entered STN: 13 Dec 2007
Last Updated on STN: 13 Dec 2007

ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

AB We report a case of pyomyositis due to Mycobacterium haemophilum in a
renal transplant recipient. M. haemophilum was identified by PCR-mediated
sequence analysis of the heat shock protein gene in the DNA of the
specimen. The patient was successfully treated with repeated surgical
debridement and prolonged anti-mycobacterial therapy.

AU Jang, Eun-Young; Lee, Sang-Oh; Choi, Seong-Ho; Sung, Heungsup; Kim, Mi-Na;
Kim, Bum-Joon ; Kim, Yang Soo; Woo, Jun Hee

STP KeyWords Plus (R): GENE ***HSP65*** ; IDENTIFICATION; PATIENT; RPOB;
AVIUM; AIDS

L2 ANSWER 7 OF 15 CAPLUS COPYRIGHT 2009 ACS on STN DUPLICATE 4

AN 2007:1135732 CAPLUS <<LOGINID::20090617>>

DN 148:281748

TI Outbreak of Mycobacterium massiliense infection associated with
intramuscular injections

AU Kim, Hee-Young; Yun, Yeo-Jun; Park, Chan Geun; Lee, Dong Han; Cho, Yong
Kyun; Park, Byung Joo; Joo, Sae-Ick; Kim, Eui-Chong; Hur, Young Joo;
Kim, Bum-Joon ; Kook, Yoon-Hoh

CS Department of Microbiology, Cancer Research Institute, Institute of
Endemic Diseases, SNUMRC, S. Korea

SO Journal of Clinical Microbiology (2007), 45(9), 3127-3130
CODEN: JCMIDW; ISSN: 0095-1137

PB American Society for Microbiology
 DT Journal
 LA English

AB Twelve strains of a rapidly growing Mycobacterium species were isolated from an outbreak assocd. with i.m. injections of an antimicrobial agent and were identified by comparative sequence anal. of rpoB and ***hsp65***. These isolates were identified as Mycobacterium massiliense (100% similarity).

RE.CNT 12 THERE ARE 12 CITED REFERENCES AVAILABLE FOR THIS RECORD
 ALL CITATIONS AVAILABLE IN THE RE FORMAT

AU . . . Yeo-Jun; Park, Chan Geun; Lee, Dong Han; Cho, Yong Kyun; Park, Byung Joo; Joo, Sae-Ick; Kim, Eui-Chong; Hur, Young Joo; ***Kim,***
 *** Bum-Joon***; Kook, Yoon-Hoh

AB . . . an outbreak assocd. with i.m. injections of an antimicrobial agent and were identified by comparative sequence anal. of rpoB and ***hsp65***. These isolates were identified as Mycobacterium massiliense (100% similarity).

ST Mycobacterium infection ribostamycin intramuscular injection antibiotic susceptibility; gene sequence rpoB ***hsp65*** Mycobacterium infection taxonomy epidemiol

IT Heat-shock proteins
 RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
 (***HSP*** 65, gene ***hsp65***; outbreak of Mycobacterium massiliense infection assocd. with i.m. injections)

IT Gene, microbial
 RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
 (***hsp65***; outbreak of Mycobacterium massiliense infection assocd. with i.m. injections)

IT Evolution
 (mol., rpoB and ***hsp65*** sequence phylogeny; outbreak of Mycobacterium massiliense infection assocd. with i.m. injections)

L2 ANSWER 8 OF 15 SCISEARCH COPYRIGHT (c) 2009 The Thomson Corporation on STN

AN 2007:1211730 SCISEARCH <<LOGINID::20090617>>

GA The Genuine Article (R) Number: 228MD

TI Pulmonary disease caused by Mycobacterium xenopi: The first case in Korea

AU Koh, Won-Jung (Reprint)

CS Sungkyunkwan Univ, Sch Med, Samsung Med Ctr, Dept Med, Div Pulm & Crit Care Med, 50 Irwan Dong, Seoul, South Korea (Reprint)

AU Park, Hye Yun; Kwon, O. Jung; Lee, Nam Yong; Shim, Young Mog; Park, Young Kil; Bai, Gill Han; Mun, Ho-Suk; ***Kim, Bum-Joon***

CS Sungkyunkwan Univ, Sch Med, Samsung Med Ctr, Dept Med, Div Pulm & Crit Care Med, Seoul, South Korea; Sungkyunkwan Univ, Sch Med, Samsung Med Ctr, Dept Lab Med, Seoul, South Korea; Sungkyunkwan Univ, Sch Med, Samsung Med Ctr, Dept Thorac Surg, Seoul, South Korea; Korean Natl TB Assoc, Korean Inst TB, Seoul, South Korea; Seoul Natl Univ, Coll Med, Dept Microbiol & Immunol, Seoul, South Korea; Seoul Natl Univ, Coll Med, Canc Res Inst, Seoul, South Korea
 E-mail: wjkoh@skku.edu

CYA South Korea

SO YONSEI MEDICAL JOURNAL, (31 OCT 2007) Vol. 48, No. 5, pp. 871-875.
 ISSN: 0513-5796.

PB YONSEI UNIV COLLEGE MEDICINE, C/O KYUNO-IL IM, M.D., PH.D, SHINCHON DONG 134, SEODAEMOON KU, SEOUL 120-752, SOUTH KOREA.

DT Article; Journal
 LA English
 REC Reference Count: 20
 ED Entered STN: 6 Dec 2007
 Last Updated on STN: 6 Dec 2007
 ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

AB *Mycobacterium xenopi* is a nontuberculous mycobacterium (NTM) that rarely causes pulmonary disease in Asia. Here we describe the first case of *M. xenopi* pulmonary disease in Korea. A 66-year-old man was admitted to our hospital with a 2-month history of productive cough and hemoptysis. His past medical history included pulmonary tuberculosis 44 years earlier, leading to a right upper lobectomy. Chest X-ray upon admission revealed cavitary consolidation involving the entire right lung. Numerous acid-fast bacilli were seen in his initial sputum, and *M. xenopi* was subsequently identified in more than five sputum cultures, using molecular methods. Despite treatment with clarithromycin, rifampicin, ethambutol, and streptomycin, the infiltrative shadow revealed on chest X-ray increased in size. The patient's condition worsened, and a right completion pneumonectomy was performed. The patient consequently died of respiratory failure on postoperative day 47, secondary to the development of a late bronchopleural fistula. This case serves as a reminder to clinicians that the incidence of NTM infection is increasing in Korea and that unusual NTM are capable of causing disease in non-immunocompromised patients.

AU . . Park, Hye Yun; Kwon, O. Jung; Lee, Nam Yong; Shim, Young Mog; Park, Young Kil; Bai, Gill Han; Mun, Ho-Suk; ***Kim, Bum-Joon***

STP KeyWords Plus (R): NONTUBERCULOUS MYCOBACTERIA; INFECTION; DIFFERENTIATION; CLARITHROMYCIN; SPECIMENS; PATIENT; ***HSP65*** ; GENE

L2 ANSWER 9 OF 15 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN DUPLICATE 5

AN 2007:338789 BIOSIS <<LOGINID::20090617>>

DN PREV200700342042

TI *Mycobacterium seoulense* sp nov., a slowly growing scotochromogenic species.

AU Mun, Ho-Suk; Kim, Hyun-Ju; Oh, Eun-Ju; Kim, Hong; Bai, Gil-Han; Yu, Hee-Kyung; Park, Young-Gil; Cha, Chang-Yong; Kook, Yoon-Hoh; ***Kim,***
 *** Bum-Joon*** [Reprint Author]

CS Seoul Natl Univ, Dept Microbiol and Immunol, Canc Res Inst, Coll Med, Seoul 110799, South Korea
 kbumjoon@snu.ac.kr

SO International Journal of Systematic and Evolutionary Microbiology, (MAR 2007) Vol. 57, No. Part 3, pp. 594-599.
 ISSN: 1466-5026.

DT Article
 LA English
 ED Entered STN: 6 Jun 2007
 Last Updated on STN: 6 Jun 2007

AB A. previously undescribed, slowly growing, scotochromogenic mycobacterium was isolated from a patient with symptomatic pulmonary infection during ***hsp65*** sequence-based identification of Korean clinical isolates. Phenetic characteristics of this strain were generally similar to those of *Mycobacterium nebraskense* and *Mycobacterium scrofulaceum*. However, some phenetic characteristics differentiated it from these two species. Its 16S rRNA gene sequences were unique and phylogenetic analysis based on 16S rRNA gene sequences placed the organism in the slowly growing *Mycobacterium* group close to *M. nebraskense* and *M. scrofulaceum*. Its

unique rnycolic acid profiles and the results of phylogenetic analysis based on two independent alternative chronometer molecules, ***hsp65*** and rpoB, confirmed the taxonomic status of this strain as representing a novel species. These data support the conclusion that this strain represents a novel mycobacterial species, for which the name *Mycobacterium seoulense* sp. nov. is proposed. The type strain is strain 03-19(T) (=DSM 44998(T)=KCTC 19146(T)).

AU Mun, Ho-Suk; Kim, Hyun-Ju; Oh, Eun-Ju; Kim, Hong; Bai, Gil-Han; Yu, Hee-Kyung; Park, Young-Gil; Cha, Chang-Yong; Kook, Yoon-Hoh; ***Kim,***
 *** Bum-Joon*** [Reprint Author]

AB A. previously undescribed, slowly growing, scotochromogenic mycobacterium was isolated from a patient with symptomatic pulmonary infection during ***hsp65*** sequence-based identification of Korean clinical isolates. Phenetic characteristics of this strain were generally similar to those of *Mycobacterium nebraskense* and . . . *M. scrofulaceum*. Its unique rnycolic acid profiles and the results of phylogenetic analysis based on two independent alternative chronometer molecules, ***hsp65*** and rpoB, confirmed the taxonomic status of this strain as representing a novel species. These data support the conclusion that . . .

GEN *Mycobacterium* ***hsp65*** gene [*Mycobacterium* heat shock protein 65 gene] (*Mycobacteriaceae*): expression; *Mycobacterium* rpoB gene (*Mycobacteriaceae*): expression

L2 ANSWER 10 OF 15 CAPLUS COPYRIGHT 2009 ACS ON STN
 AN 2007:465634 CAPLUS <<LOGINID:20090617>>
 DN 147:339410
 TI *Mycobacterium seoulense* sp. nov., a slowly growing scotochromogenic species

AU Mun, Ho-Suk; Kim, Hyun-Ju; Oh, Eun-Ju; Kim, Hong; Bai, Gil-Han; Yu, Hee-Kyung; Park, Young-Gil; Cha, Chang-Yong; Kook, Yoon-Hoh; ***Kim,***
 *** Bum-Joon***

CS Department of Microbiology and Immunology, Cancer Research Institute and Liver Research Institute, College of Medicine, Seoul National University, Seoul, 110-799, S. Korea

SO International Journal of Systematic and Evolutionary Microbiology (2007), 57(3), 593-599
 CODEN: ISEMF5; ISSN: 1466-5026

PB Society for General Microbiology
 DT Journal
 LA English

AB A previously undescribed, slowly growing, scotochromogenic mycobacterium was isolated from a patient with symptomatic pulmonary infection during ***hsp65*** sequence-based identification of Korean clin. isolates. Phenetic characteristics of this strain were generally similar to those of *Mycobacterium nebraskense* and *Mycobacterium scrofulaceum*. However, some phenetic characteristics differentiated it from these two species. Its 16S rRNA gene sequences were unique and phylogenetic anal. based on 16S rRNA gene sequences placed the organism in the slowly growing *Mycobacterium* group close to *M. nebraskense* and *M. scrofulaceum*. Its unique mycolic acid profiles and the results of phylogenetic anal. based on two independent alternative chronometer mols., ***hsp65*** and rpoB, confirmed the taxonomic status of this strain as representing a novel species. These data support the conclusion that this strain represents a novel mycobacterial species, for which the name *Mycobacterium seoulense* sp. nov. is proposed. The type strain is strain 03-19T (= DSM 44998T = KCTC 19146T).

RE.CNT 20 THERE ARE 20 CITED REFERENCES AVAILABLE FOR THIS RECORD

ALL CITATIONS AVAILABLE IN THE RE FORMAT

- AU Mun, Ho-Suk; Kim, Hyun-Ju; Oh, Eun-Ju; Kim, Hong; Bai, Gil-Han; Yu, Hee-Kyung; Park, Young-Gil; Cha, Chang-Yong; Kook, Yoon-Hoh; ***Kim,***
 *** Bum-Joon***
- AB A previously undescribed, slowly growing, scotochromogenic mycobacterium was isolated from a patient with symptomatic pulmonary infection during ***hsp65*** sequence-based identification of Korean clin. isolates. Phenetic characteristics of this strain were generally similar to those of *Mycobacterium nebraskense* and . . . *M. scrofulaceum*. Its unique mycolic acid profiles and the results of phylogenetic anal. based on two independent alternative chronometer mols., ***hsp65*** and *rpoB*, confirmed the taxonomic status of this strain as representing a novel species. These data support the conclusion that. . .
- ST *Mycobacterium* scotochromogenic 16S rRNA gene *rpoB* ***hsp65*** sequence
- IT Heat-shock proteins
 RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
 (***HSP*** 65; *Mycobacterium seoulense* sp. nov., a slowly growing scotochromogenic species)
- IT Gene, microbial
 RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
 (***hsp65*** ; *Mycobacterium seoulense* sp. nov., a slowly growing scotochromogenic species)
- L2 ANSWER 11 OF 15 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN DUPLICATE 6
- AN 2007:135186 BIOSIS <<LOGINID::20090617>>
- DN PREV200700134974
- TI Direct application of *Ava*II PCR restriction fragment length polymorphism analysis (*Ava*II PRA) targeting 644 bp heat shock protein 65 (***hsp65***) gene to sputum samples.
- AU Mun, Ho-Suk; Kim, Hyun-Ju; Oh, Eun-Ju; Kim, Hong; Park, Young-Gil; Bai, Gil-Han; Do, Junghwan; Cha, Chang-Yong; Kook, Yoon-Hoh; ***Kim,***
 *** Bum-Joon*** [Reprint Author]
- CS Seoul Natl Univ, Coll Med, Dept Microbiol, 28 Yongon Dong, Seoul 110799, South Korea
 kbumjoon@snu.ac.kr
- SO Microbiology and Immunology, (2007) Vol. 51, No. 1, pp. 105-110.
 CODEN: MIIMDV. ISSN: 0385-5600.
- DT Article
 LA English
 ED Entered STN: 22 Feb 2007
 Last Updated on STN: 22 Feb 2007
- AB To evaluate the usefulness of the *Ava*II PRA method targeting 644-bp ***hsp65*** gene for the direct detection of pathogenic mycobacteria from clinical specimens, we applied this method to 40 sputum samples and compared the results to those obtained by IS6110 PCR. Although this method showed a sensitivity slightly lower than IS6110 PCR (97.5% vs. 100%), it detected infections of *M. avium* complex (MAC) in two patients, which was not possible by IS6110 PCR. We conclude that *Ava*II PRA is a highly effective method for directly detecting pathogenic mycobacteria in primary clinical specimens.
- TI Direct application of *Ava*II PCR restriction fragment length polymorphism analysis (*Ava*II PRA) targeting 644 bp heat shock protein 65 (***hsp65***) gene to sputum samples.
- AU Mun, Ho-Suk; Kim, Hyun-Ju; Oh, Eun-Ju; Kim, Hong; Park, Young-Gil; Bai,

Gill-Han; Do, Junghwan; Cha, Chang-Yong; Kook, Yoon-Hoh; ***Kim,***
 *** Bum-Joon*** [Reprint Author]

AB To evaluate the usefulness of the *Ava*II PRA method targeting 644-bp
 hsp65 gene for the direct detection of pathogenic mycobacteria
 from clinical specimens, we applied this method to 40 sputum samples and
 . . .

GEN *Mycobacterium avium* ***hsp65*** gene [*Mycobacterium avium* heat shock
 protein 65 gene] (*Mycobacteriaceae*): expression; *Mycobacterium*
tuberculosis ***hsp65*** gene [*Mycobacterium tuberculosis* heat shock
 protein 65 gene] (*Mycobacteriaceae*): expression

L2 ANSWER 12 OF 15 CAPLUS COPYRIGHT 2009 ACS on STN DUPLICATE 7
 AN 2006:1304935 CAPLUS <<LOGINID::20090617>>
 DN 146:515458

TI Differentiation of mycobacterial species by ***hsp65*** duplex PCR
 followed by duplex-PCR-based restriction analysis and direct sequencing

AU Kim, Hyun-Ju; Mun, Ho-Suk; Kim, Hong; Oh, Eun-Ju; Ha, Youngju; Bai,
 Gill-Han; Park, Young-Gil; Cha, Chang-Yong; Kook, Yoon-Hoh; ***Kim,***
 *** Bum-Joon***

CS Department of Microbiology and Immunology, Cancer Research Institute and
 Liver Research Institute, College of Medicine, Seoul National University,
 Seoul, 110-799, S. Korea

SO Journal of Clinical Microbiology (2006), 44(11), 3855-3862
 CODEN: JCMIDW; ISSN: 0095-1137

PB American Society for Microbiology
 DT Journal
 LA English

AB Here we describe a novel duplex PCR method which can differentiate
Mycobacterium tuberculosis and nontuberculosis mycobacteria (NTM) strains
 by amplifying ***hsp65*** DNAs of different sizes (195 and 515 bp,
 resp.). The devised technique was applied to 54 ref. and 170 clin.
 isolates and differentiated all strains into their resp. groups with 100%
 sensitivity and specificity. Furthermore, a duplex PCR-restriction anal.
 (duplex PRA) and a direct sequencing protocol were developed to
 differentiate NTM strains at the species and subspecies levels based on
 previously reported ***hsp65*** DNA sequences and then applied to 105
 NTM clin. isolates. All NTM isolates were clearly differentiated at the
 species and subspecies levels by subsequent procedures (PRA or direct
 sequencing) targeting 515-bp NTM duplex PCR amplicons. Our results
 suggest that novel duplex PCR-based methods are sensitive and specific for
 identifying mycobacterial culture isolates at the species level.

RE.CNT 25 THERE ARE 25 CITED REFERENCES AVAILABLE FOR THIS RECORD
 ALL CITATIONS AVAILABLE IN THE RE FORMAT

TI Differentiation of mycobacterial species by ***hsp65*** duplex PCR
 followed by duplex-PCR-based restriction analysis and direct sequencing

AU Kim, Hyun-Ju; Mun, Ho-Suk; Kim, Hong; Oh, Eun-Ju; Ha, Youngju; Bai,
 Gill-Han; Park, Young-Gil; Cha, Chang-Yong; Kook, Yoon-Hoh; ***Kim,***
 *** Bum-Joon***

AB Here we describe a novel duplex PCR method which can differentiate
Mycobacterium tuberculosis and nontuberculosis mycobacteria (NTM) strains
 by amplifying ***hsp65*** DNAs of different sizes (195 and 515 bp,
 resp.). The devised technique was applied to 54 ref. and 170 clin. . . .
 a direct sequencing protocol were developed to differentiate NTM strains
 at the species and subspecies levels based on previously reported
 hsp65 DNA sequences and then applied to 105 NTM clin. isolates.
 All NTM isolates were clearly differentiated at the species and. . .

ST *Mycobacterium* species differentiation ***hsp65*** duplex PCR

restriction analysis sequencing
 IT DNA sequence analysis
 Mycobacterium tuberculosis
 Tuberculosis
 (differentiation of mycobacterial species by ***hsp65*** duplex PCR
 followed by duplex-PCR-based restriction anal. and direct sequencing)
 IT Primers (nucleic acid)
 RL: ARG (Analytical reagent use); DGN (Diagnostic use); PRP (Properties);
 ANST (Analytical study); BIOL (Biological study); USES (Uses)
 (differentiation of mycobacterial species by ***hsp65*** duplex PCR
 followed by duplex-PCR-based restriction anal. and direct sequencing)
 IT Genetic methods
 (duplex-PCR-based restriction anal.; differentiation of mycobacterial
 species by ***hsp65*** duplex PCR followed by duplex-PCR-based
 restriction anal. and direct sequencing)
 IT Polymerase chain reaction
 (duplex; differentiation of mycobacterial species by ***hsp65***
 duplex PCR followed by duplex-PCR-based restriction anal. and direct
 sequencing)
 IT Gene, microbial
 RL: ANT (Analyte); DGN (Diagnostic use); ANST (Analytical study); BIOL
 (Biological study); USES (Uses)
 (***hsp65*** ; differentiation of mycobacterial species by
 hsp65 duplex PCR followed by duplex-PCR-based restriction
 anal.
 and direct sequencing)
 IT Human
 (isolates from; differentiation of mycobacterial species by
 hsp65 duplex PCR followed by duplex-PCR-based restriction
 anal.
 and direct sequencing)
 IT Diagnosis
 (mol.; differentiation of mycobacterial species by ***hsp65***
 duplex PCR followed by duplex-PCR-based restriction anal. and direct
 sequencing)
 IT Mycobacterium
 (nontuberculosis; differentiation of mycobacterial species by
 hsp65 duplex PCR followed by duplex-PCR-based restriction
 anal.
 and direct sequencing)
 IT 936858-56-9 936858-57-0 936858-58-1 936858-59-2 936858-60-5
 936858-61-6 936858-62-7 936858-64-9 936858-65-0
 RL: ARG (Analytical reagent use); DGN (Diagnostic use); PRP (Properties);
 ANST (Analytical study); BIOL (Biological study); USES (Uses)
 (primer; differentiation of mycobacterial species by ***hsp65***
 duplex PCR followed by duplex-PCR-based restriction anal. and direct
 sequencing)
 L2 ANSWER 13 OF 15 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on
 STN DUPLICATE 8
 AN 2005:448449 BIOSIS <LOGINID::20090617>
 DN PREV200510237956
 TI Differentiation of Mycobacterium species by analysis of the heat-shock
 protein 65 gene (***hsp65***).
 AU Kim, Hong; Kim, Sun-Hyun; Shim, Tae-Sun; Kim, Mi-na; Bai, Gill-Han; Park,
 Young-Gil; Lee, Sueng-Hyun; Chae, Gue-Tae; Cha, Chang-Yong; Kook,
 Yoon-Hoh; ***Kim, Bum-Joon*** [Reprint Author]

CS Seoul Natl Univ, Coll Med, Dept Microbiol, 28 Yongon Dong, Seoul 110799,
South Korea
kbumjoon@snu.ac.kr

SO International Journal of Systematic and Evolutionary Microbiology, (JUL
2005) Vol. 55, No. Part 4, pp. 1649-1656.
ISSN: 1466-5026.

DT Article
LA English
ED Entered STN: 3 Nov 2005
Last Updated on STN: 3 Nov 2005

AB The nucleotide sequences (604 bp) of partial heat-shock protein genes (
hsp65) from 161 Mycobacterium strains containing 56 reference
Mycobacterium species and 105 clinical isolates were determined and
compared. ***hsp65*** sequence analysis showed a higher degree of
divergence between Mycobacterium species than did 16S rRNA gene analysis.
Generally, the topology of the phylogenetic tree based on the
hsp65 DNA sequences was similar to that of the 16S rRNA gene,
thus revealing natural relationships among Mycobacterium species. When a
direct sequencing protocol targeting 422 bp sequences was applied to 70
non-tuberculous mycobacterium (NTM) clinical isolates, all NTMs were
clearly identified. In addition, an XhoI PCR restriction fragment length
polymorphism analysis method for the differentiation of Mycobacterium,
tuberculosis complex from NTM strains was developed during this study.
The results obtained suggest that 604 bp ***hsp65*** sequences are
useful for the phylogenetic analysis and species identification of
mycobacteria.

TI Differentiation of Mycobacterium species by analysis of the heat-shock
protein 65 gene (***hsp65***).

AU. . . Kim, Hong; Kim, Sun-Hyun; Shim, Tae-Sun; Kim, Mi-na; Bai, Gill-Han;
Park, Young-Gil; Lee, Sueng-Hyun; Chae, Gue-Tae; Cha, Chang-Yong; Kook,
Yoon-Hoh; ***Kim, Bum-Joon*** [Reprint Author]

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hsp65) from 161 Mycobacterium strains containing 56 reference
Mycobacterium species and 105 clinical isolates were determined and
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divergence between Mycobacterium species than did 16S rRNA gene analysis.
Generally, the topology of the phylogenetic tree based on the
hsp65 DNA sequences was similar to that of the 16S rRNA gene,
thus revealing natural relationships among Mycobacterium species. When a . .
. differentiation of Mycobacterium, tuberculosis complex from NTM strains
was developed during this study. The results obtained suggest that 604 bp
hsp65 sequences are useful for the phylogenetic analysis and
species identification of mycobacteria.

IT . . .
Genetics (Population Studies); Systematics and Taxonomy

IT Chemicals & Biochemicals
16S rRNA [16S ribosomal RNA]; endonuclease; heat shock protein 65 [
HSP65]

GEN Mycobacterium 16S rRNA gene (Mycobacteriaceae); Mycobacterium
hsp65 gene [Mycobacterium heat-shock protein 65 gene gene]
(Mycobacteriaceae)

L2 ANSWER 14 OF 15 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on
STN DUPLICATE 9

AN 2005:437869 BIOSIS <<LOGINID::20090617>>

DN PREV200510224308
 TI PCR restriction fragment length polymorphism analysis (PRA)-algorithm targeting 644 bp Heat Shock Protein 65 (***hsp65***) gene for differentiation of Mycobacterium spp.
 AU Kim, Hong; Kim, Sun-Hyun; Shim, Tae-Sun; Kim, Mi-na; Bai, Gill-Han; Park, Young-Gil; Lee, Sueng-Hyun; Cha, Chang-Yong; Kook, Yoon-Hoh; ***Kim,***
 *** Bum-Joon*** [Reprint Author]
 CS Seoul Natl Univ, Coll Med, Dept Microbiol, 28 Yongon Dong, Seoul 110799, South Korea
 kbumjoon@snu.ac.kr
 SO Journal of Microbiological Methods, (AUG 2005) Vol. 62, No. 2, pp. 199-209.
 CODEN: JMICDQ. ISSN: 0167-7012.
 DT Article
 LA English
 ED Entered STN: 26 Oct 2005
 Last Updated on STN: 26 Oct 2005
 AB A method based on PCR-restriction fragment length polymorphism analysis (PRA) using a novel region of the ***hsp65*** gene was developed for the rapid and exact identification of mycobacteria to the species level. A 644 bp region of ***hsp65*** in 62 mycobacteria reference strains, and 4 related bacterial strains were amplified, and the amplified DNAs were subsequently digested with restriction enzymes, namely, *Ava*II, *Hph*I, and *Hpa*II. Most of the mycobacteria species were easily differentiated at the species level by the developed method. In particular, the method enabled the separation of *M. avium*, *M. intracellulare* and *M. tuberculosis* to the species level by *Ava*II digestion alone. An algorithm was constructed based on the results and a blind test was successfully performed on 251 clinical isolates, which had been characterized by conventional biochemical testing. Our results suggest that this novel PRA offers a simple, rapid, and accurate method for the identification of mycobacteria culture isolates at the species level. (c) 2005 Elsevier B.V. All rights reserved.
 TI PCR restriction fragment length polymorphism analysis (PRA)-algorithm targeting 644 bp Heat Shock Protein 65 (***hsp65***) gene for differentiation of Mycobacterium spp.
 AU Kim, Hong; Kim, Sun-Hyun; Shim, Tae-Sun; Kim, Mi-na; Bai, Gill-Han; Park, Young-Gil; Lee, Sueng-Hyun; Cha, Chang-Yong; Kook, Yoon-Hoh; ***Kim,***
 *** Bum-Joon*** [Reprint Author]
 AB A method based on PCR-restriction fragment length polymorphism analysis (PRA) using a novel region of the ***hsp65*** gene was developed for the rapid and exact identification of mycobacteria to the species level. A 644 bp region of ***hsp65*** in 62 mycobacteria reference strains, and 4 related bacterial strains were amplified, and the amplified DNAs were subsequently digested with. . .
 GEN Mycobacterium ***hsp65*** gene [Mycobacterium heat shock protein 65 gene] (Mycobacteriaceae)
 L2 ANSWER 15 OF 15 CAPLUS COPYRIGHT 2009 ACS on STN
 AN 2003:591378 CAPLUS <<LOGINID:20090617>>
 DN 139:146183
 TI Primers for amplifying mycobacterial heat shock protein ***HSP*** 65 gene and use for identifying mycobacterial species
 IN ***Kim, Bum-joon*** ; Kook, Yoon-ho; Kim, Jeong-mi
 PA Biomedlab Corporation, S. Korea
 SO PCT Int. Appl., 102 pp.
 CODEN: PIXXD2

DT Patent
LA English
FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 2003062470	A1	20030731	WO 2003-KR131	20030121
	W:	AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW			
	RW:	GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG			
	KR 2003063935	A	20030731	KR 2002-4297	20020124
	KR 2003072087	A	20030913	KR 2002-11648	20020305
	US 20050014157	A1	20050120	US 2004-500586	20040909
PRAI	KR 2002-4297	A	20020124		
	KR 2002-11648	A	20020305		
	WO 2003-KR131	W	20030121		
AB	The present invention relates to a pair of primers specific to mycobacterial species, a polynucleotide of an ***HSP*** 65 gene fragment, and a method for the identification of mycobacterial species by using the same. More specifically, the 604-bp ***HSP*** 65 gene fragment can be applied to identification methods of mycobacteria such as the comparative sequence anal. method, the probe hybridization method, and PCR-RFLP, which can resolve the problems of a conventional identification method based on biochem. characteristics, where the genus mycobacterium covers various species and has a low growth rate, and of the problems of 16s rDNA. Thus, according to the identification method of the present invention, the mycobacterial species can be identified simply, economically, and accurately.				
RE.CNT 5	THERE ARE 5 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT				
TI	Primers for amplifying mycobacterial heat shock protein ***HSP*** 65 gene and use for identifying mycobacterial species				
IN	***Kim, Bum-joon*** ; Kook, Yoon-ho; Kim, Jeong-mi				
AB	The present invention relates to a pair of primers specific to mycobacterial species, a polynucleotide of an ***HSP*** 65 gene fragment, and a method for the identification of mycobacterial species by using the same. More specifically, the 604-bp ***HSP*** 65 gene fragment can be applied to identification methods of mycobacteria such as the comparative sequence anal. method, the probe. . .				
ST	primer mycobacteria heat shock protein ***hsp65*** gene				
IT	Nucleic acid amplification (method) (DNA); primers for amplifying mycobacterial heat shock protein ***HSP*** 65 gene and use for identifying mycobacterial species)				
IT	Heat-shock proteins RL: ARG (Analytical reagent use); BPN (Biosynthetic preparation); BSU (Biological study, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); PREP (Preparation); USES (Uses) (***HSP*** 65; primers for amplifying mycobacterial heat shock protein ***HSP*** 65 gene and use for identifying mycobacterial species)				

IT Gene, microbial
 RL: ARG (Analytical reagent use); BSU (Biological study, unclassified);
 DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL
 (Biological study); USES (Uses)
 (***HSP*** 65; primers for amplifying mycobacterial heat shock
 protein ***HSP*** 65 gene and use for identifying mycobacterial
 species)

IT Diagnosis
 (mol.; primers for amplifying mycobacterial heat shock protein
 HSP 65 gene and use for identifying mycobacterial species)

IT DNA sequences
 Mycobacterium
 Mycobacterium BCG
 Mycobacterium abscessus
 Mycobacterium africanum
 Mycobacterium aichiense
 Mycobacterium asiaticum
 Mycobacterium avium
 Mycobacterium avium paratuberculosis
 Mycobacterium bovis
 Mycobacterium celatum
 Mycobacterium chelonae
 Mycobacterium chitae
 Mycobacterium farcinogenes
 Mycobacterium flavescens
 Mycobacterium fortuitum
 Mycobacterium gastri
 Mycobacterium genavense
 Mycobacterium gordonae
 Mycobacterium haemophilum
 Mycobacterium interjectum
 Mycobacterium intracellulare
 Mycobacterium kansasii
 Mycobacterium leprae
 Mycobacterium malmoense
 Mycobacterium marinum
 Mycobacterium microti
 Mycobacterium mucogenicum
 Mycobacterium neoaurum
 Mycobacterium nonchromogenicum
 Mycobacterium parafortuitum
 Mycobacterium peregrinum
 Mycobacterium phlei
 Mycobacterium scrofulaceum
 Mycobacterium senegalense
 Mycobacterium shimoidei
 Mycobacterium simiae
 Mycobacterium smegmatis
 Mycobacterium szulgai
 Mycobacterium terrae
 Mycobacterium thermoresistibile
 Mycobacterium triviale
 Mycobacterium tuberculosis
 Mycobacterium ulcerans
 Mycobacterium vaccae
 Mycobacterium wolinskyi
 Nocardia carnea

RFLP (restriction fragment length polymorphism)
Tsukamurella paurometabola
Tsukamurella pulmonis
Tsukamurella tyrosinosolvens
(primers for amplifying mycobacterial heat shock protein ***HSP***
65 gene and use for identifying mycobacterial species)

IT Primers (nucleic acid)
RL: ARG (Analytical reagent use); BPN (Biosynthetic preparation); BSU (Biological study, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); PREP (Preparation); USES (Uses)
(primers for amplifying mycobacterial heat shock protein ***HSP***
65 gene and use for identifying mycobacterial species)

IT 569430-56-4 569432-08-2 569432-09-3 569432-10-6 569432-11-7
569432-12-8 569432-13-9 569432-14-0 569432-15-1 569432-16-2
569432-17-3 569432-18-4 569432-19-5 569432-20-8 569432-21-9
569432-22-0 569432-23-1 569432-24-2 569432-25-3 569432-26-4
569432-27-5 569432-28-6 569432-29-7 569432-30-0 569432-31-1
569432-32-2 569432-33-3 569432-34-4 569432-35-5 569432-36-6
569432-37-7 569432-38-8 569432-39-9 569432-40-2 569432-41-3
569432-42-4 569432-43-5 569432-44-6 569432-45-7 569432-46-8
569432-47-9 569432-48-0 569432-49-1 569432-50-4 569432-51-5
569432-52-6 569432-53-7 569432-54-8 569432-55-9
RL: ARG (Analytical reagent use); BSU (Biological study, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(nucleotide sequence; primers for amplifying mycobacterial heat shock protein ***HSP*** 65 gene and use for identifying mycobacterial species)

IT 569432-56-0
RL: ARG (Analytical reagent use); BSU (Biological study, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(primer ***HSPF3*** sequence; primers for amplifying mycobacterial heat shock protein ***HSP*** 65 gene and use for identifying mycobacterial species)

IT 569432-57-1
RL: ARG (Analytical reagent use); BSU (Biological study, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(primer ***HSPR3*** sequence; primers for amplifying mycobacterial heat shock protein ***HSP*** 65 gene and use for identifying mycobacterial species)

IT 81295-43-4, Nuclease, restriction endonuclease, Xho I
RL: BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
(primers for amplifying mycobacterial heat shock protein ***HSP*** 65 gene and use for identifying mycobacterial species)

IT 569477-29-8
RL: PRP (Properties)
(unclaimed sequence; primers for amplifying mycobacterial heat shock protein ***HSP*** 65 gene and use for identifying mycobacterial species)

=> e kook yoon ho/au

E1 3 KOOK YOON BUM/AU

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E2      1      KOOK YOON HAWN/AU
E3      4 --> KOOK YOON HO/AU
E4      288    KOOK YOON HOH/AU
E5      1      KOOK YOON HOH DR/AU
E6      1      KOOK YOON HOH*/AU
E7      10     KOOK YOON HWAN/AU
E8      3      KOOK YOON SANG/AU
E9      1      KOOK YOONAH/AU
E10     1      KOOK YOONBUM/AU
E11     1      KOOK YOONHO/AU
E12     14     KOOK YOONHOH/AU

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=> s e3-e6 and hsp?

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L3      45 ("KOOK YOON HO"/AU OR "KOOK YOON HOH"/AU OR "KOOK YOON HOH DR"/A
        U OR "KOOK YOON HOH*/AU) AND HSP?

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=> dup rem l3

PROCESSING COMPLETED FOR L3

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L4      11 DUP REM L3 (34 DUPLICATES REMOVED)

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=> d bib ab kwic 1-

YOU HAVE REQUESTED DATA FROM 11 ANSWERS - CONTINUE? Y/(N):y

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L4      ANSWER 1 OF 11 CAPLUS COPYRIGHT 2009 ACS on STN DUPLICATE 1

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AN      2008:1298911 CAPLUS <<LOGINID::20090617>>

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TI      Proportions of Mycobacterium massiliense and Mycobacterium bollettii
        strains among Korean Mycobacterium chelonae-Mycobacterium abscessus group
        isolates

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AU      Kim, Hee-Young; Kook, Yoonwon; Yun, Yeo-Jun; Park, Chan Geun; Lee, Nam
        Yong; Shim, Tae Sun; Kim, Bum-Joon; ***Kook, Yoon-Hoh***

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CS      Department of Microbiology, Cancer Research Institute, Institute of
        Endemic Diseases, SNUMRC, and Clinical Research Institute, Seoul National
        University College of Medicine, Seoul National University Hospital, Seoul,
        110-799, S. Korea

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SO      Journal of Clinical Microbiology (2008), 46(10), 3384-3390

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        CODEN: JCMIDW; ISSN: 0095-1137

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PB      American Society for Microbiology

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DT      Journal

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LA      English

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AB      Korean isolates of the Mycobacterium chelonae-Mycobacterium abscessus
        group, which had been isolated from two different hospitals in South
        Korea, were identified by PCR restriction anal. (PRA) and comparative
        sequence anal. of 16S rRNA genes, rpoB, and ***hsp65*** to evaluate
        the proportion of four closely related species (M. chelonae, M. abscessus,
        M. massiliense, and M. bollettii). Of the 144 rapidly growing
        mycobacterial strains tested, 127 strains (88.2%) belonged to the M.
        chelonae-M. abscessus group. In this group, M. chelonae, M. abscessus, M.
        massiliense, and M. bollettii accounted for 0.8% (n = 1), 51.2% (n = 65),
        46.5% (n = 59), and 1.6% (n = 2), resp. Two isolates which showed
        discordant results, M. massiliense by rpoB sequence anal. and M. abscessus
        by ***hsp65*** sequence anal., were finally identified as M.
        massiliense based on the addnl. anal. of sodA and the 16S-23S internal
        transcribed spacer. M. abscessus group I isolates previously identified
        by ***hsp65*** PRA were all found to be M. abscessus, whereas group II
        isolates were further identified as M. massiliense or M. bollettii by
        sequencing of rpoB and ***hsp65***. Smooth, rough, or mixed colonies

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of both *M. abscessus* and *M. massiliense* isolates were obsd. *M. massiliense* strains that were highly resistant to clarithromycin had a point mutation at the adenine at position 2058 (A2058) or 2059 (A2059) in the peptidyltransferase region of the 23S rRNA gene.

RE.CNT 42 THERE ARE 42 CITED REFERENCES AVAILABLE FOR THIS RECORD

ALL CITATIONS AVAILABLE IN THE RE FORMAT

AU Kim, Hee-Young; Kook, Yoonwon; Yun, Yeo-Jun; Park, Chan Geun; Lee, Nam Young; Shim, Tae Sun; Kim, Bum-Joon; ***Kook, Yoon-Hoh***

AB . . . in South Korea, were identified by PCR restriction anal. (PRA) and comparative sequence anal. of 16S rRNA genes, rpoB, and ***hsp65*** to evaluate the proportion of four closely related species (*M. chelonae*, *M. abscessus*, *M. massiliense*, and *M. bolletii*). Of the. . . (n = 2), resp. Two isolates which showed discordant results, *M. massiliense* by rpoB sequence anal. and *M. abscessus* by ***hsp65*** sequence anal., were finally identified as *M. massiliense* based on the addnl. anal. of sodA and the 16S-23S internal transcribed spacer. *M. abscessus* group I isolates previously identified by ***hsp65*** PRA were all found to be *M. abscessus*, whereas group II isolates were further identified as *M. massiliense* or *M. bolletii* by sequencing of rpoB and ***hsp65***. Smooth, rough, or mixed colonies of both *M. abscessus* and *M. massiliense* isolates were obsd. *M. massiliense* strains that were. . .

ST Mycobacterium ***hsp65*** rpoB 16S rRNA gene

IT INDEXING IN PROGRESS

IT INDEXING IN PROGRESS

IT Human
Mycobacterium abscessus
Mycobacterium bolletii
Mycobacterium chelonae
Mycobacterium massiliense
(*M. chelonae*-*M. abscessus* group isolate from Korean patient show high prevalence of *M. massiliense*, *M. abscessus* and *M. massiliense*, *M. bolletii* accounted for *M. abscessus* group II strains identified by ***hsp65*** PCR restriction anal.)

L4 ANSWER 2 OF 11 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN DUPLICATE 2

AN 2008:322988 BIOSIS <LOGINID::20090617>

DN PREV200800322987

TI Mycobacterium sensuense sp nov., a slowly growing, non-chromogenic species closely related to the Mycobacterium terrae complex.

AU Mun, Ho-Suk; Park, Joo-Hee; Kim, Hong; Yu, Hee-Kyung; Park, Young-Gil; Cha, Chang-Yong; ***Kook, Yoon-Hoh*** ; Kim, Bum-Joon [Reprint Author]

CS Seoul Natl Univ, Coll Med, Dept Microbiol and Immunol, Canc Res Inst, Seoul 110799, South Korea
kbumjoon@snu.ac.kr

SO International Journal of Systematic and Evolutionary Microbiology, (MAR 2008) Vol. 58, No. Part 3, pp. 641-646.
ISSN: 1466-5026.

DT Article

LA English

OS GenBank-DQ536407; EMBL-DQ536407; DDJB-DQ536407; GenBank-DQ536409; EMBL-DQ536409; DDJB-DQ536409

ED Entered STN: 29 May 2008
Last Updated on STN: 29 May 2008

AB A previously undescribed, slowly growing, non-chromogenic mycobacterium, isolated from a Korean patient with a symptomatic pulmonary infection, is described as representing a novel species. Its 16S rRNA gene sequence was

unique and phylogenetic analysis based on 16S rRNA gene sequences showed that this organism belonged to the *Mycobacterium terrae* subclade. Phenotypically, the strain was generally similar to *M. terrae* and *Mycobacterium nonchromogenicum*, but its growth rate was slower than those of other *M. terrae* complex strains. A unique mycolic acid profile and phylogenetic analysis based on two different alternative chronometer molecules, ***hsp65*** and *rpoB*, confirm the taxonomic status of this strain as a representative of a novel species. The name *Mycobacterium sensu* sp. nov. is proposed, with the type strain 05-832(T) (=DSM 44999(T) =KCTC 19147(T)).

AU Mun, Ho-Suk; Park, Joo-Hee; Kim, Hong; Yu, Hee-Kyung; Park, Young-Gil; Cha, Chang-Yong; ***Kook, Yoon-Hoh*** ; Kim, Bum-Joon [Reprint Author]

AB. . . other *M. terrae* complex strains. A unique mycolic acid profile and phylogenetic analysis based on two different alternative chronometer molecules, ***hsp65*** and *rpoB*, confirm the taxonomic status of this strain as a representative of a novel species. The name *Mycobacterium sensu* sp. nov. is proposed, with the type strain 05-832(T) (=DSM 44999(T) =KCTC 19147(T)).

IT Major Concepts

IT Chemicals & Biochemicals
rpoB; ***hsp65*** ; 16S ribosomal RNA [16S rRNA, gene sequence]

L4 ANSWER 3 OF 11 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN DUPLICATE 3

AN 2008:636733 BIOSIS <<LOGINID::20090617>>

DN PREV200800636732

TI Differentiation of mycobacteria in sputa by duplex polymerase chain reaction for mycobacterial ***hsp65*** gene.

AU Kim, Bum-Joon [Reprint Author]; Park, Joo-Hee; Lee, Seoung-Ae; Kim, Hong; Cha, Chang-Yong; ***Kook, Yoon-Hoh*** ; Kim, Eui-Chong; Joo, Sei Ick; Lee, Jae Seok; Yim, Jae-Joon

CS Seoul Natl Univ, Coll Med, Canc Res Inst, Dept Microbiol and Immunol, Seoul 110744, South Korea
 kbumjoon@snu.ac.kr; yimjj@snu.ac.kr

SO Diagnostic Microbiology and Infectious Disease, (OCT 2008) Vol. 62, No. 2, pp. 193-198.
 CODEN: DMIDDZ. ISSN: 0732-8893.

DT Article

LA English

ED Entered STN: 19 Nov 2008
 Last Updated on STN: 19 Nov 2008

AB Early differentiation of mycobacteria in Sputa is crucial. This study was set to evaluate the usefulness of a newly developed duplex polymerase chain reaction (PCR) for ***hsp65*** gene-based method in differentiating mycobacteria in sputum with a positive acid-fast bacilli (AFB) smear before culturing. One hundred forty-seven sputa with positive AFB smear were included for the analysis. *Mycobacterium* species identified using a newly developed duplex PCR for ***hsp65*** gene followed by a nested PCR-direct were sequencing and the conventional colony-based method. Final decision of mycobacterial species were made based on 1) results of species identification based on mycobacterial colonies or 2) results of species identification of other sputa from the same patients and clinical findings. The duplex PCR-based method correctly identified 83.2% Sputa from tuberculosis patients and 82.2% sputa from nontuberculous mycobacteria patients, whereas the colonybased method correctly identified 86.1% and 77.8%, respectively. Sensitivity and specificity of the colony-based method for *Mycobacterium tuberculosis*

were 86.1% and 100%, respectively, whereas those of the duplex PCR-based method were 83.2% and 95.6%, respectively. The duplex PCR-based method, to differentiate mycobacterial species in Sputa, produced comparable results as those of the colony-based identification method. (C) 2008 Elsevier Inc. All rights reserved.

TI Differentiation of mycobacteria in sputa by duplex polymerase chain reaction for mycobacterial ***hsp65*** gene.

AU Kim, Bum-Joon [Reprint Author]; Park, Joo-Hee; Lee, Seoung-Ae; Kim, Hong; Cha, Chang-Yong; ***Kook, Yoon-Hoh*** ; Kim, Eui-Chong; Joo, Sei Ick; Lee, Jae Seok; Yim, Jae-Joon

AB. . . is crucial. This study was set to evaluate the usefulness of a newly developed duplex polymerase chain reaction (PCR) for ***hsp65*** gene-based method in differentiating mycobacteria in sputum with a positive acid-fast bacilli (AFB) smear before culturing. One hundred forty-seven sputa with positive AFB smear were included for the analysis. Mycobacterial species identified using a newly developed duplex PCR for ***hsp65*** gene followed by a nested PCR-direct were sequencing and the conventional colony-based method. Final decision of mycobacterial species were made. . .

GEN Mycobacterium ***hsp65*** gene (Mycobacteriaceae)

L4 ANSWER 4 OF 11 CAPLUS COPYRIGHT 2009 ACS on STN DUPLICATE 4

AN 2007:1135732 CAPLUS <<LOGINID::20090617>>

DN 148:281748

TI Outbreak of Mycobacterium massiliense infection associated with intramuscular injections

AU Kim, Hee-Young; Yun, Yeo-Jun; Park, Chan Geun; Lee, Dong Han; Cho, Yong Kyun; Park, Byung Joo; Joo, Sae-Ick; Kim, Eui-Chong; Hur, Young Joo; Kim, Bum-Joon; ***Kook, Yoon-Hoh***

CS Department of Microbiology, Cancer Research Institute, Institute of Endemic Diseases, SNUMRC, S. Korea

SO Journal of Clinical Microbiology (2007), 45(9), 3127-3130

CODEN: JCMIDW; ISSN: 0095-1137

PB American Society for Microbiology

DT Journal

LA English

AB Twelve strains of a rapidly growing Mycobacterium species were isolated from an outbreak assocd. with i.m. injections of an antimicrobial agent and were identified by comparative sequence anal. of rpoB and ***hsp65***. These isolates were identified as Mycobacterium massiliense (100% similarity).

RE.CNT 12 THERE ARE 12 CITED REFERENCES AVAILABLE FOR THIS RECORD

ALL CITATIONS AVAILABLE IN THE RE FORMAT

AU . . . Chan Geun; Lee, Dong Han; Cho, Yong Kyun; Park, Byung Joo; Joo, Sae-Ick; Kim, Eui-Chong; Hur, Young Joo; Kim, Bum-Joon; ***Kook,***

*** Yoon-Hoh***

AB . . . an outbreak assocd. with i.m. injections of an antimicrobial agent and were identified by comparative sequence anal. of rpoB and ***hsp65***. These isolates were identified as Mycobacterium massiliense (100% similarity).

ST Mycobacterium infection ribostamycin intramuscular injection antibiotic susceptibility; gene sequence rpoB ***hsp65*** Mycobacterium infection taxonomy epidemiol

IT Heat-shock proteins

RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)

(***HSP*** 65, gene ***hsp65*** ; outbreak of Mycobacterium massiliense infection assocd. with i.m. injections)

IT Gene, microbial
 RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
 (***hsp65*** ; outbreak of Mycobacterium massiliense infection assocd. with i.m. injections)

IT Evolution
 (mol., rpoB and ***hsp65*** sequence phylogeny; outbreak of Mycobacterium massiliense infection assocd. with i.m. injections)

L4 ANSWER 5 OF 11 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN DUPLICATE 5

AN 2007:338789 BIOSIS <<LOGINID::20090617>>

DN PREV200700342042

TI Mycobacterium seoulense sp nov., a slowly growing scotochromogenic species.

AU Mun, Ho-Suk; Kim, Hyun-Ju; Oh, Eun-Ju; Kim, Hong; Bai, Gil-Han; Yu, Hee-Kyung; Park, Young-Gil; Cha, Chang-Yong; ***Kook, Yoon-Hoh*** ; Kim, Bum-Joon [Reprint Author]

CS Seoul Natl Univ, Dept Microbiol and Immunol, Canc Res Inst, Coll Med, Seoul 110799, South Korea
 kbumjoon@snu.ac.kr

SO International Journal of Systematic and Evolutionary Microbiology, (MAR 2007) Vol. 57, No. Part 3, pp. 594-599.
 ISSN: 1466-5026.

DT Article
 LA English
 ED Entered STN: 6 Jun 2007
 Last Updated on STN: 6 Jun 2007

AB A. previously undescribed, slowly growing, scotochromogenic mycobacterium was isolated from a patient with symptomatic pulmonary infection during ***hsp65*** sequence-based identification of Korean clinical isolates. Phenetic characteristics of this strain were generally similar to those of Mycobacterium nebraskense and Mycobacterium scrofulaceum. However, some phenetic characteristics differentiated it from these two species. Its 16S rRNA gene sequences were unique and phylogenetic analysis based on 16S rRNA gene sequences placed the organism in the slowly growing Mycobacterium group close to M. nebraskense and M. scrofulaceum. Its unique rnycolic acid profiles and the results of phylogenetic analysis based on two independent alternative chronometer molecules, ***hsp65*** and rpoB, confirmed the taxonomic status of this strain as representing a novel species. These data support the conclusion that this strain represents a novel mycobacterial species, for which the name Mycobacterium seoulense sp. nov. is proposed. The type strain is strain 03-19(T) (=DSM 44998(T)=KCTC 19146(T)).

AU Mun, Ho-Suk; Kim, Hyun-Ju; Oh, Eun-Ju; Kim, Hong; Bai, Gil-Han; Yu, Hee-Kyung; Park, Young-Gil; Cha, Chang-Yong; ***Kook, Yoon-Hoh*** ; Kim, Bum-Joon [Reprint Author]

AB A. previously undescribed, slowly growing, scotochromogenic mycobacterium was isolated from a patient with symptomatic pulmonary infection during ***hsp65*** sequence-based identification of Korean clinical isolates. Phenetic characteristics of this strain were generally similar to those of Mycobacterium nebraskense and . . . M. scrofulaceum. Its unique rnycolic acid profiles and the results of phylogenetic analysis based on two independent alternative chronometer molecules, ***hsp65*** and rpoB, confirmed the taxonomic status of this strain as representing a

novel species. These data support the conclusion that. . .

GEN Mycobacterium ***hsp65*** gene [Mycobacterium heat shock protein 65 gene] (Mycobacteriaceae): expression; Mycobacterium rpoB gene (Mycobacteriaceae): expression

L4 ANSWER 6 OF 11 CAPLUS COPYRIGHT 2009 ACS on STN

AN 2007:465634 CAPLUS <<LOGINID::20090617>>

DN 147:339410

TI Mycobacterium seoulense sp. nov., a slowly growing scotochromogenic species

AU Mun, Ho-Suk; Kim, Hyun-Ju; Oh, Eun-Ju; Kim, Hong; Bai, Gil-Han; Yu, Hee-Kyung; Park, Young-Gil; Cha, Chang-Yong; ***Kook, Yoon-Hoh*** ; Kim, Bum-Joon

CS Department of Microbiology and Immunology, Cancer Research Institute and Liver Research Institute, College of Medicine, Seoul National University, Seoul, 110-799, S. Korea

SO International Journal of Systematic and Evolutionary Microbiology (2007), 57(3), 593-599

CODEN: ISEMF5; ISSN: 1466-5026

PB Society for General Microbiology

DT Journal

LA English

AB A previously undescribed, slowly growing, scotochromogenic mycobacterium was isolated from a patient with symptomatic pulmonary infection during ***hsp65*** sequence-based identification of Korean clin. isolates. Phenetic characteristics of this strain were generally similar to those of Mycobacterium nebraskense and Mycobacterium scrofulaceum. However, some phenetic characteristics differentiated it from these two species. Its 16S rRNA gene sequences were unique and phylogenetic anal. based on 16S rRNA gene sequences placed the organism in the slowly growing Mycobacterium group close to M. nebraskense and M. scrofulaceum. Its unique mycolic acid profiles and the results of phylogenetic anal. based on two independent alternative chronometer mols., ***hsp65*** and rpoB, confirmed the taxonomic status of this strain as representing a novel species. These data support the conclusion that this strain represents a novel mycobacterial species, for which the name Mycobacterium seoulense sp. nov. is proposed. The type strain is strain 03-19T (= DSM 44998T = KCTC 19146T).

RE.CNT 20 THERE ARE 20 CITED REFERENCES AVAILABLE FOR THIS RECORD

ALL CITATIONS AVAILABLE IN THE RE FORMAT

AU Mun, Ho-Suk; Kim, Hyun-Ju; Oh, Eun-Ju; Kim, Hong; Bai, Gil-Han; Yu, Hee-Kyung; Park, Young-Gil; Cha, Chang-Yong; ***Kook, Yoon-Hoh*** ; Kim, Bum-Joon

AB A previously undescribed, slowly growing, scotochromogenic mycobacterium was isolated from a patient with symptomatic pulmonary infection during ***hsp65*** sequence-based identification of Korean clin. isolates. Phenetic characteristics of this strain were generally similar to those of Mycobacterium nebraskense and. . . M. scrofulaceum. Its unique mycolic acid profiles and the results of phylogenetic anal. based on two independent alternative chronometer mols., ***hsp65*** and rpoB, confirmed the taxonomic status of this strain as representing a novel species. These data support the conclusion that. . .

ST Mycobacterium scotochromogenic 16S rRNA gene rpoB ***hsp65*** sequence

IT Heat-shock proteins

RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)

(***HSP*** 65; Mycobacterium seoulense sp. nov., a slowly growing

scotochromogenic species)

IT Gene, microbial
 RL: BSU (Biological study, unclassified); PRP (Properties); BIOL
 (Biological study)
 (***hsp65*** ; Mycobacterium seoulense sp. nov., a slowly growing
 scotochromogenic species)

L4 ANSWER 7 OF 11 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN
 DUPLICATE 6

AN 2007:135186 BIOSIS <<LOGINID::20090617>>

DN PREV200700134974

TI Direct application of *Ava*II PCR restriction fragment length polymorphism
 analysis (*Ava*II PRA) targeting 644 bp heat shock protein 65 (***hsp65***
) gene to sputum samples.

AU Mun, Ho-Suk; Kim, Hyun-Ju; Oh, Eun-Ju; Kim, Hong; Park, Young-Gil; Bai,
 Gil-Han; Do, Junghwan; Cha, Chang-Yong; ***Kook, Yoon-Hoh*** ; Kim,
 Bum-Joon [Reprint Author]

CS Seoul Natl Univ, Coll Med, Dept Microbiol, 28 Yongon Dong, Seoul 110799,
 South Korea
 kbumjoon@snu.ac.kr

SO Microbiology and Immunology, (2007) Vol. 51, No. 1, pp. 105-110.
 CODEN: MIIMDV. ISSN: 0385-5600.

DT Article

LA English

ED Entered STN: 22 Feb 2007
 Last Updated on STN: 22 Feb 2007

AB To evaluate the usefulness of the *Ava*II PRA method targeting 644-bp
 hsp65 gene for the direct detection of pathogenic mycobacteria
 from clinical specimens, we applied this method to 40 sputum samples and
 compared the results to those obtained by IS6110 PCR. Although this
 method showed a sensitivity slightly lower than IS6110 PCR (97.5% vs.
 100%), it detected infections of *M. avium* complex (MAC) in two patients,
 which was not possible by IS6110 PCR. We conclude that *Ava*II PRA is a
 highly effective method for directly detecting pathogenic mycobacteria in
 primary clinical specimens.

TI Direct application of *Ava*II PCR restriction fragment length polymorphism
 analysis (*Ava*II PRA) targeting 644 bp heat shock protein 65 (***hsp65***
) gene to sputum samples.

AU Mun, Ho-Suk; Kim, Hyun-Ju; Oh, Eun-Ju; Kim, Hong; Park, Young-Gil; Bai,
 Gil-Han; Do, Junghwan; Cha, Chang-Yong; ***Kook, Yoon-Hoh*** ; Kim,
 Bum-Joon [Reprint Author]

AB To evaluate the usefulness of the *Ava*II PRA method targeting 644-bp
 hsp65 gene for the direct detection of pathogenic mycobacteria
 from clinical specimens, we applied this method to 40 sputum samples and.
 .

GEN Mycobacterium avium ***hsp65*** gene [Mycobacterium avium heat shock
 protein 65 gene] (Mycobacteriaceae): expression; Mycobacterium
 tuberculosis ***hsp65*** gene [Mycobacterium tuberculosis heat shock
 protein 65 gene] (Mycobacteriaceae): expression

L4 ANSWER 8 OF 11 CAPLUS COPYRIGHT 2009 ACS on STN DUPLICATE 7

AN 2006:1304935 CAPLUS <<LOGINID::20090617>>

DN 146:515458

TI Differentiation of mycobacterial species by ***hsp65*** duplex PCR
 followed by duplex-PCR-based restriction analysis and direct sequencing

AU Kim, Hyun-Ju; Mun, Ho-Suk; Kim, Hong; Oh, Eun-Ju; Ha, Youngju; Bai,
 Gill-Han; Park, Young-Gil; Cha, Chang-Yong; ***Kook, Yoon-Hoh*** ; Kim,

Bum-Joon

CS Department of Microbiology and Immunology, Cancer Research Institute and Liver Research Institute, College of Medicine, Seoul National University, Seoul, 110-799, S. Korea

SO Journal of Clinical Microbiology (2006), 44(11), 3855-3862
CODEN: JCMIDW; ISSN: 0095-1137

PB American Society for Microbiology

DT Journal

LA English

AB Here we describe a novel duplex PCR method which can differentiate Mycobacterium tuberculosis and nontuberculosis mycobacteria (NTM) strains by amplifying ***hsp65*** DNAs of different sizes (195 and 515 bp, resp.). The devised technique was applied to 54 ref. and 170 clin. isolates and differentiated all strains into their resp. groups with 100% sensitivity and specificity. Furthermore, a duplex PCR-restriction anal. (duplex PRA) and a direct sequencing protocol were developed to differentiate NTM strains at the species and subspecies levels based on previously reported ***hsp65*** DNA sequences and then applied to 105 NTM clin. isolates. All NTM isolates were clearly differentiated at the species and subspecies levels by subsequent procedures (PRA or direct sequencing) targeting 515-bp NTM duplex PCR amplicons. Our results suggest that novel duplex PCR-based methods are sensitive and specific for identifying mycobacterial culture isolates at the species level.

RE.CNT 25 THERE ARE 25 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

TI Differentiation of mycobacterial species by ***hsp65*** duplex PCR followed by duplex-PCR-based restriction analysis and direct sequencing

AU Kim, Hyun-Ju; Mun, Ho-Suk; Kim, Hong; Oh, Eun-Ju; Ha, Youngju; Bai, Gill-Han; Park, Young-Gil; Cha, Chang-Yong; ***Kook, Yoon-Hoh*** ; Kim, Bum-Joon

AB Here we describe a novel duplex PCR method which can differentiate Mycobacterium tuberculosis and nontuberculosis mycobacteria (NTM) strains by amplifying ***hsp65*** DNAs of different sizes (195 and 515 bp, resp.). The devised technique was applied to 54 ref. and 170 clin. . . . a direct sequencing protocol were developed to differentiate NTM strains at the species and subspecies levels based on previously reported ***hsp65*** DNA sequences and then applied to 105 NTM clin. isolates. All NTM isolates were clearly differentiated at the species and. . .

ST Mycobacterium species differentiation ***hsp65*** duplex PCR restriction analysis sequencing

IT DNA sequence analysis
Mycobacterium tuberculosis
Tuberculosis
(differentiation of mycobacterial species by ***hsp65*** duplex PCR followed by duplex-PCR-based restriction anal. and direct sequencing)

IT Primers (nucleic acid)
RL: ARG (Analytical reagent use); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(differentiation of mycobacterial species by ***hsp65*** duplex PCR followed by duplex-PCR-based restriction anal. and direct sequencing)

IT Genetic methods
(duplex-PCR-based restriction anal.; differentiation of mycobacterial species by ***hsp65*** duplex PCR followed by duplex-PCR-based restriction anal. and direct sequencing)

IT Polymerase chain reaction
(duplex; differentiation of mycobacterial species by ***hsp65*** duplex PCR followed by duplex-PCR-based restriction anal. and direct

sequencing)
IT Gene, microbial
RL: ANT (Analyte); DGN (Diagnostic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(***hsp65*** ; differentiation of mycobacterial species by
hsp65 duplex PCR followed by duplex-PCR-based restriction
anal.
and direct sequencing)
IT Human
(isolate from; differentiation of mycobacterial species by
hsp65 duplex PCR followed by duplex-PCR-based restriction
anal.
and direct sequencing)
IT Diagnosis
(mol.; differentiation of mycobacterial species by ***hsp65***
duplex PCR followed by duplex-PCR-based restriction anal. and direct
sequencing)
IT Mycobacterium
(nontuberculosis; differentiation of mycobacterial species by
hsp65 duplex PCR followed by duplex-PCR-based restriction
anal.
and direct sequencing)
IT 936858-56-9 936858-57-0 936858-58-1 936858-59-2 936858-60-5
936858-61-6 936858-62-7 936858-64-9 936858-65-0
RL: ARG (Analytical reagent use); DGN (Diagnostic use); PRP (Properties);
ANST (Analytical study); BIOL (Biological study); USES (Uses)
(primer; differentiation of mycobacterial species by ***hsp65***
duplex PCR followed by duplex-PCR-based restriction anal. and direct
sequencing)
L4 ANSWER 9 OF 11 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN
DUPLICATE 8
AN 2005:448449 BIOSIS <<LOGINID::20090617>>
DN PREV200510237956
TI Differentiation of Mycobacterium species by analysis of the heat-shock
protein 65 gene (***hsp65***).
AU Kim, Hong; Kim, Sun-Hyun; Shim, Tae-Sun; Kim, Mi-na; Bai, Gill-Han; Park,
Young-Gil; Lee, Sueng-Hyun; Chae, Gue-Tae; Cha, Chang-Yong; ***Kook,***
*** Yoon-Hoh*** ; Kim, Bum-Joon [Reprint Author]
CS Seoul Natl Univ, Coll Med, Dept Microbiol, 28 Yongon Dong, Seoul 110799,
South Korea
kbumjoon@snu.ac.kr
SO International Journal of Systematic and Evolutionary Microbiology, (JUL
2005) Vol. 55, No. Part 4, pp. 1649-1656.
ISSN: 1466-5026.
DT Article
LA English
ED Entered STN: 3 Nov 2005
Last Updated on STN: 3 Nov 2005
AB The nucleotide sequences (604 bp) of partial heat-shock protein genes (
hsp65) from 161 Mycobacterium strains containing 56 reference
Mycobacterium species and 105 clinical isolates were determined and
compared. ***hsp65*** sequence analysis showed a higher degree of
divergence between Mycobacterium species than did 16S rRNA gene analysis.
Generally, the topology of the phylogenetic tree based on the
hsp65 DNA sequences was similar to that of the 16S rRNA gene,
thus

revealing natural relationships among Mycobacterium species. When a direct sequencing protocol targeting 422 bp sequences was applied to 70 non-tuberculous mycobacterium (NTM) clinical isolates, all NTMs were clearly identified. In addition, an XhoI PCR restriction fragment length polymorphism analysis method for the differentiation of Mycobacterium, tuberculosis complex from NTM strains was developed during this study. The results obtained suggest that 604 bp ***hsp65*** sequences are useful for the phylogenetic analysis and species identification of mycobacteria.

TI Differentiation of Mycobacterium species by analysis of the heat-shock protein 65 gene (***hsp65***).

AU Kim, Hong; Kim, Sun-Hyun; Shim, Tae-Sun; Kim, Mi-na; Bai, Gill-Han; Park, Young-Gil; Lee, Sueng-Hyun; Chae, Gue-Tae; Cha, Chang-Yong; ***Kook,***

*** Yoon-Hoh*** ; Kim, Bum-Joon [Reprint Author]

AB The nucleotide sequences (604 bp) of partial heat-shock protein genes (***hsp65***) from 161 Mycobacterium strains containing 56 reference Mycobacterium species and 105 clinical isolates were determined and compared. ***hsp65*** sequence analysis showed a higher degree of divergence between Mycobacterium species than did 16S rRNA gene analysis. Generally, the topology of the phylogenetic tree based on the ***hsp65*** DNA sequences was similar to that of the 16S rRNA gene,

thus revealing natural relationships among Mycobacterium species. When a . . . differentiation of Mycobacterium, tuberculosis complex from NTM strains was developed during this study. The results obtained suggest that 604 bp ***hsp65*** sequences are useful for the phylogenetic analysis and species identification of mycobacteria.

II . . .

II Genetics (Population Studies); Systematics and Taxonomy

II Chemicals & Biochemicals

16S rRNA [16S ribosomal RNA]; endonuclease; heat shock protein 65 [***HSP65***]

GEN Mycobacterium 16S rRNA gene (Mycobacteriaceae); Mycobacterium ***hsp65*** gene [Mycobacterium heat-shock protein 65 gene gene] (Mycobacteriaceae)

L4 ANSWER 10 OF 11 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN DUPLICATE 9

AN 2005:437869 BIOSIS <LOGINID:20090617>

DN PREV200510224308

TI PCR restriction fragment length polymorphism analysis (PRA)-algorithm targeting 644 bp Heat Shock Protein 65 (***hsp65***) gene for differentiation of Mycobacterium spp.

AU Kim, Hong; Kim, Sun-Hyun; Shim, Tae-Sun; Kim, Mi-na; Bai, Gill-Han; Park, Young-Gil; Lee, Sueng-Hyun; Cha, Chang-Yong; ***Kook, Yoon-Hoh*** ; Kim, Bum-Joon [Reprint Author]

CS Seoul Natl Univ, Coll Med, Dept Microbiol, 28 Yongon Dong, Seoul 110799, South Korea
kbumjoon@snu.ac.kr

SO Journal of Microbiological Methods, (AUG 2005) Vol. 62, No. 2, pp. 199-209.
CODEN: JMI MQ. ISSN: 0167-7012.

DT Article

LA English

ED Entered STN: 26 Oct 2005
Last Updated on STN: 26 Oct 2005

AB A method based on PCR-restriction fragment length polymorphism analysis

(PRA) using a novel region of the ***hsp65*** gene was developed for the rapid and exact identification of mycobacteria to the species level. A 644 bp region of ***hsp65*** in 62 mycobacteria reference strains, and 4 related bacterial strains were amplified, and the amplified DNAs were subsequently digested with restriction enzymes, namely, *Ava*II, *Hph*I, and *Hpa*II. Most of the mycobacteria species were easily differentiated at the species level by the developed method. In particular, the method enabled the separation of *M. avium*, *M. intracellulare* and *M. tuberculosis* to the species level by *Ava*II digestion alone. An algorithm was constructed based on the results and a blind test was successfully performed on 251 clinical isolates, which had been characterized by conventional biochemical testing. Our results suggest that this novel PRA offers a simple, rapid, and accurate method for the identification of mycobacteria culture isolates at the species level. (c) 2005 Elsevier B.V. All rights reserved.

TI PCR restriction fragment length polymorphism analysis (PRA)-algorithm targeting 644 bp Heat Shock Protein 65 (***hsp65***) gene for differentiation of *Mycobacterium* spp.

AB Kim, Hong; Kim, Sun-Hyun; Shim, Tae-Sun; Kim, Mi-na; Bai, Gill-Han; Park, Young-Gil; Lee, Sueng-Hyun; Cha, Chang-Yong; ***Kook, Yoon-Hoh*** ; Kim, Bum-Joon [Reprint Author]

AB A method based on PCR-restriction fragment length polymorphism analysis (PRA) using a novel region of the ***hsp65*** gene was developed for the rapid and exact identification of mycobacteria to the species level. A 644 bp region of ***hsp65*** in 62 mycobacteria reference strains, and 4 related bacterial strains were amplified, and the amplified DNAs were subsequently digested with. . .

GEN *Mycobacterium* ***hsp65*** gene [*Mycobacterium* heat shock protein 65 gene] (*Mycobacteriaceae*)

L4 ANSWER 11 OF 11 CAPLUS COPYRIGHT 2009 ACS on STN

AN 2003:591378 CAPLUS <<LOGINID:20090617>>

DN 139:146183

TI Primers for amplifying mycobacterial heat shock protein ***HSP*** 65 gene and use for identifying mycobacterial species

IN Kim, Bum-joon; ***Kook, Yoon-ho*** ; Kim, Jeong-mi

PA Biomedlab Corporation, S. Korea

SO PCT Int. Appl., 102 pp.

CODEN: PIXXD2

DT Patent

LA English

FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 2003062470	A1	20030731	WO 2003-KR131	20030121
	W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW				
	RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG				
	KR 2003063935	A	20030731	KR 2002-4297	20020124
	KR 2003072087	A	20030913	KR 2002-11648	20020305

	US 20050014157	A1	20050120	US 2004-500586	20040909
PRAI	KR 2002-4297	A	20020124		
	KR 2002-11648	A	20020305		
	WO 2003-KR131	W	20030121		

AB The present invention relates to a pair of primers specific to mycobacterial species, a polynucleotide of an ***HSP*** 65 gene fragment, and a method for the identification of mycobacterial species by using the same. More specifically, the 604-bp ***HSP*** 65 gene fragment can be applied to identification methods of mycobacteria such as the comparative sequence anal. method, the probe hybridization method, and PCR-RFLP, which can resolve the problems of a conventional identification method based on biochem. characteristics, where the genus mycobacterium covers various species and has a low growth rate, and of the problems of 16s rDNA. Thus, according to the identification method of the present invention, the mycobacterial species can be identified simply, economically, and accurately.

RE.CNT 5 THERE ARE 5 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

TI Primers for amplifying mycobacterial heat shock protein ***HSP*** 65 gene and use for identifying mycobacterial species

IN Kim, Bum-joon; ***Kook, Yoon-ho*** ; Kim, Jeong-mi

AB The present invention relates to a pair of primers specific to mycobacterial species, a polynucleotide of an ***HSP*** 65 gene fragment, and a method for the identification of mycobacterial species by using the same. More specifically, the 604-bp ***HSP*** 65 gene fragment can be applied to identification methods of mycobacteria such as the comparative sequence anal. method, the probe. . .

ST primer mycobacteria heat shock protein ***hsp65*** gene

IT Nucleic acid amplification (method)
(DNA; primers for amplifying mycobacterial heat shock protein
HSP 65 gene and use for identifying mycobacterial species)

IT Heat-shock proteins
RL: ARG (Analytical reagent use); BPN (Biosynthetic preparation); BSU (Biological study, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); PREP (Preparation); USES (Uses)
(***HSP*** 65; primers for amplifying mycobacterial heat shock protein ***HSP*** 65 gene and use for identifying mycobacterial species)

IT Gene, microbial
RL: ARG (Analytical reagent use); BSU (Biological study, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(***HSP*** 65; primers for amplifying mycobacterial heat shock protein ***HSP*** 65 gene and use for identifying mycobacterial species)

IT Diagnosis
(mol.; primers for amplifying mycobacterial heat shock protein
HSP 65 gene and use for identifying mycobacterial species)

IT DNA sequences
Mycobacterium
Mycobacterium BCG
Mycobacterium abscessus
Mycobacterium africanum
Mycobacterium aichiense
Mycobacterium asiaticum
Mycobacterium avium

Mycobacterium avium paratuberculosis
 Mycobacterium bovis
 Mycobacterium celatum
 Mycobacterium chelonae
 Mycobacterium chitae
 Mycobacterium farcinogenes
 Mycobacterium flavescens
 Mycobacterium fortuitum
 Mycobacterium gastri
 Mycobacterium genavense
 Mycobacterium gordonae
 Mycobacterium haemophilum
 Mycobacterium interjectum
 Mycobacterium intracellulare
 Mycobacterium kansasii
 Mycobacterium leprae
 Mycobacterium malmoense
 Mycobacterium marinum
 Mycobacterium microti
 Mycobacterium mucogenicum
 Mycobacterium neoaurum
 Mycobacterium nonchromogenicum
 Mycobacterium parafortuitum
 Mycobacterium peregrinum
 Mycobacterium phlei
 Mycobacterium scrofulaceum
 Mycobacterium senegalense
 Mycobacterium shimoidei
 Mycobacterium simiae
 Mycobacterium smegmatis
 Mycobacterium szulgai
 Mycobacterium terrae
 Mycobacterium thermoresistibile
 Mycobacterium triviale
 Mycobacterium tuberculosis
 Mycobacterium ulcerans
 Mycobacterium vaccae
 Mycobacterium wolinskyi
 Nocardia carnea
 RFLP (restriction fragment length polymorphism)
 Tsukamurella paurometabola
 Tsukamurella pulmonis
 Tsukamurella tyrosinosolvens
 (primers for amplifying mycobacterial heat shock protein ***HSP***
 65 gene and use for identifying mycobacterial species)
 IT Primers (nucleic acid)
 RL: ARG (Analytical reagent use); BPN (Biosynthetic preparation); BSU
 (Biological study, unclassified); DGN (Diagnostic use); PRP (Properties);
 ANST (Analytical study); BIOL (Biological study); PREP (Preparation); USES
 (Uses)
 (primers for amplifying mycobacterial heat shock protein ***HSP***
 65 gene and use for identifying mycobacterial species)
 IT 569430-56-4 569432-08-2 569432-09-3 569432-10-6 569432-11-7
 569432-12-8 569432-13-9 569432-14-0 569432-15-1 569432-16-2
 569432-17-3 569432-18-4 569432-19-5 569432-20-8 569432-21-9
 569432-22-0 569432-23-1 569432-24-2 569432-25-3 569432-26-4
 569432-27-5 569432-28-6 569432-29-7 569432-30-0 569432-31-1

569432-32-2 569432-33-3 569432-34-4 569432-35-5 569432-36-6
569432-37-7 569432-38-8 569432-39-9 569432-40-2 569432-41-3
569432-42-4 569432-43-5 569432-44-6 569432-45-7 569432-46-8
569432-47-9 569432-48-0 569432-49-1 569432-50-4 569432-51-5
569432-52-6 569432-53-7 569432-54-8 569432-55-9
RL: ARG (Analytical reagent use); BSU (Biological study, unclassified);
DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL
(Biological study); USES (Uses)
(nucleotide sequence; primers for amplifying mycobacterial heat shock
protein ***HSP*** 65 gene and use for identifying mycobacterial
species)
IT 569432-56-0
RL: ARG (Analytical reagent use); BSU (Biological study, unclassified);
DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL
(Biological study); USES (Uses)
(primer ***HSPF3*** sequence; primers for amplifying mycobacterial
heat shock protein ***HSP*** 65 gene and use for identifying
mycobacterial species)
IT 569432-57-1
RL: ARG (Analytical reagent use); BSU (Biological study, unclassified);
DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL
(Biological study); USES (Uses)
(primer ***HSPR3*** sequence; primers for amplifying mycobacterial
heat shock protein ***HSP*** 65 gene and use for identifying
mycobacterial species)
IT 81295-43-4, Nuclease, restriction endodeoxyribo-, Xho I
RL: BUU (Biological use, unclassified); BIOL (Biological study); USES
(Uses)
(primers for amplifying mycobacterial heat shock protein ***HSP***
65 gene and use for identifying mycobacterial species)
IT 569477-29-8
RL: PRP (Properties)
(unclaimed sequence; primers for amplifying mycobacterial heat shock
protein ***HSP*** 65 gene and use for identifying mycobacterial
species)

=> e kim jeong mi/au
E1 1 KIM JEONG MANN/AU
E2 30 KIM JEONG MEE/AU
E3 150 --> KIM JEONG MI/AU
E4 464 KIM JEONG MIN/AU
E5 2 KIM JEONG MM/AU
E6 15 KIM JEONG MO/AU
E7 4 KIM JEONG MOG/AU
E8 39 KIM JEONG MOK/AU
E9 1 KIM JEONG MONG/AU
E10 16 KIM JEONG MOOG/AU
E11 5 KIM JEONG MOOK/AU
E12 3 KIM JEONG MOON/AU

=> s e2-e4 and hsp?
L5 33 ("KIM JEONG MEE"/AU OR "KIM JEONG MI"/AU OR "KIM JEONG MIN"/AU)
AND HSP?

=> dup rem 15
PROCESSING COMPLETED FOR L5

=> d bib ab kwic 1-

YOU HAVE REQUESTED DATA FROM 5 ANSWERS - CONTINUE? Y/(N):y

L6 ANSWER 1 OF 5 CAPLUS COPYRIGHT 2009 ACS on STN

AN 2008:42683 CAPLUS <<LOGINID::20090617>>

DN 148:71211

TI Epilepsy diagnostic kit for diagnosing epilepsy via expression degree of epilepsy marker genes

IN Kim, Nam Sun; Jung, So Yeong; Wang, Ae Guk; Oh, Jeong Hwa; Byun, Sang Sun; ***Kim, Jeong Min*** ; Lee, Dong Seok; Jung, Cheon Gi; Lee, Yun Jin

PA Korea Research Institute of Bioscience and Biotechnology, S. Korea

SO Repub. Korean Kongkae Taeho Kongbo, 29pp.

CODEN: KRXXA7

DT Patent

LA Korean

FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
	-----	----	-----	-----	-----
PI	KR 2007116555	A	20071210	KR 2007-54409	20070604
	KR 900764	B1	20090602		
PRAI	KR 2006-50227	A	20060605		

AB The title epilepsy diagnostic kit can diagnose epilepsy via expression degree of epilepsy marker genes, including GAPDH, TSC22, TTR, DEPP, SPP1, ACTG2, ID2, HNLF, CPE, MBP, LDHA, ***HSPA9B***, A2BP1, PPP2CA, ATP6VE1, MAP2, MGC8685, HLA-C, ARF1 and VSNL1. The epilepsy diagnostic kit contains: (1) the above genes, (2) probes of 200bp complementary to the above genes, and (3) more than one of sense primers and sequences of antisense primers of the above genes.

IN Kim, Nam Sun; Jung, So Yeong; Wang, Ae Guk; Oh, Jeong Hwa; Byun, Sang Sun; ***Kim, Jeong Min*** ; Lee, Dong Seok; Jung, Cheon Gi; Lee, Yun Jin

AB . . . epilepsy via expression degree of epilepsy marker genes, including GAPDH, TSC22, TTR, DEPP, SPP1, ACTG2, ID2, HNLF, CPE, MBP, LDHA, ***HSPA9B***, A2BP1, PPP2CA, ATP6VE1, MAP2, MGC8685, HLA-C, ARF1 and VSNL1. The epilepsy diagnostic kit contains: (1) the above genes, (2) probes. . .

IT Gene, animal

RL: BSU (Biological study, unclassified); DGN (Diagnostic use); BIOL (Biological study); USES (Uses)

(***HSPA9B*** ; epilepsy diagnostic kit for diagnosing epilepsy via expression degree of epilepsy marker genes)

L6 ANSWER 2 OF 5 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN DUPLICATE 1

AN 2007:363762 BIOSIS <<LOGINID::20090617>>

DN PREV200700362958

TI Valproic acid-mediated neuroprotection in intracerebral hemorrhage via histone deacetylase inhibition and transcriptional activation.

AU Sinn, Dong-In; Kim, Se-Jeong; Chu, Kon; Jung, Keun-Hwa; Lee, Soon-Tae; Song, Eun-Cheol; ***Kim, Jeong-Min*** ; Park, Dong-Kyu; Lee, Sang Kun; Kim, Manho; Roh, Jae-Kyu [Reprint Author]

CS Seoul Natl Univ Hosp, Dept Neurol, SNUMRC, Stroke and Neural Stem Cell Lab, Neurosci Res Inst, Clin Res Inst, Stem Cell Res Ctr, 28, Yongong Dong, Seoul 110744, South Korea
rohjk@snu.ac.kr

SO Neurobiology of Disease, (MAY 2007) Vol. 26, No. 2, pp. 464-472.
ISSN: 0969-9961.

DT Article

LA English

ED Entered STN: 20 Jun 2007
Last Updated on STN: 20 Jun 2007

AB The modification of histone N-terminal tails by acetylation or deacetylation can alter the interaction between histones and DNA, and thus regulate gene expression. Recent experiments have demonstrated that valproic acid (VPA), a well-known anti-epileptic drug, can directly inhibit histone deacetylase (HDAC) activity and cause the by hyperacetylation of histones. Moreover, VPA has been shown to mediate neuronal protection by activating signal transduction pathways and by inhibiting proapoptotic factors. In this study, we attempted to determine whether VPA alleviates cerebral inflammation and perihematomal cell death after intracerebral hemorrhage (ICH). Adult male rats received intraperitoneal injections of 300 mg/kg VPA or PBS twice a day after ICH induction. VPA treatment inhibited hematoma expansion, perihematomal cell death, caspase activities, and inflammatory cell infiltration. In addition, VPA treatment had the following expressional effects; it activated the translations of acetylated histone H3, pERK, pAKT, pCREB, and ***HSP70***; up-regulated bcl-2 and bcl-xl but down-regulated bax; and down-regulated the mRNAs of Fas-L, IL-6, MMP-9, MIP-1, MCP-J, and tPA. VPA-treated rats also showed better functional recovery from 1 day to 4 weeks after ICH. Here we show that VPA induces neuroprotection in a murine ICH model and that its neuroprotective effects are mediated by transcriptional activation following HDAC inhibition. (c) 2007 Elsevier Inc. All rights reserved.

AU Sinn, Dong-In; Kim, Se-Jeong; Chu, Kon; Jung, Keun-Hwa; Lee, Soon-Tae; Song, Eun-Cheol; ***Kim, Jeong-Min***; Park, Dong-Kyu; Lee, Sang Kun; Kim, Manho; Roh, Jae-Kyu [Reprint Author]

AB. . . addition, VPA treatment had the following expressional effects; it activated the translations of acetylated histone H3, pERK, pAKT, pCREB, and ***HSP70***; up-regulated bcl-2 and bcl-xl but down-regulated bax; and down-regulated the mRNAs of Fas-L, IL-6, MMP-9, MIP-1, MCP-J, and tPA. VPA-treated. . .

IT . . .
intracerebral hemorrhage: vascular disease, nervous system disease, drug therapy
Cerebral Hemorrhage (MeSH)

IT Chemicals & Biochemicals
DNA; IL-6 [interleukin-6]; bcl-2; MCP-1; ***HSP70*** [heat shock protein 70]; H3 histone; caspase [EC 3.4.22.36]: inhibition; tPA; bax; pERK; bcl-xl; pCREB; MMP-9 [EC 3.4.24.35]; pAKT; MIP-1; . . .

L6 ANSWER 3 OF 5 CAPLUS COPYRIGHT 2009 ACS on STN

AN 2005:14598 CAPLUS <<LOGINID:20090617>>

DN 142:111833

TI Expressed sequence tags identifying marker genes for the diagnosis of gastric cancer and metastatic gastric cancer

IN Kim, Nam-Soon; Kim, Yong Sung; Lee, Ju-Yeon; Oh, Jung-Hwa; Park, Hong-Seog; Ahn, Hee-Young; Yoon, Sun-Young; Han, Yoonsoo; Kim, Sangsoo; ***Kim, Jeong-Min***; Byun, Sang-Soon; Noh, Seung-Moo; Song, Kyu-Sang; Yoo, Hyang Sook

PA Korea Research Institute of Bioscience and Biotechnology, S. Korea

SO PCT Int. Appl., 112 pp.
CODEN: PIXXD2

DT Patent
LA English
FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 2005001126	A1	20050106	WO 2004-KR677	20040325
	<p>W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BW, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, GR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MY, NA, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW</p> <p>RW: BW, GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PL, PT, RO, SE, SI, SK, TR, BF, BJ, BG, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG</p>				
	KR 2004107145	A	20041220	KR 2003-38034	20030612
	KR 2005050295	A	20050531	KR 2003-84001	20031125
	JP 2006526998	T	20061130	JP 2006-516902	20040325
PRAI	KR 2003-38034	A	20030612		
	KR 2003-84001	A	20031125		
	WO 2004-KR677	W	20040325		
AB	<p>A panel of expressed sequence tags (ESTs) that can be used as markers to diagnose gastric cancer and its metastases is identified. The genes can also be used as markers in screening for drugs for treatment of the disease (no data.). The genes from which these markers are derived are identified. Reagents for detecting expression of these genes can be incorporated into a diagnostic kit. The ESTs were identified by comparing patterns of gene expression in 12 gastric cancer cell lines and four non-cancerous gastric cell lines. Up- and down-regulated genes were identified.</p>				
RE.CNT 7	<p>THERE ARE 7 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT</p>				
IN	<p>Kim, Nam-Soon; Kim, Yong Sung; Lee, Ju-Yeon; Oh, Jung-Hwa; Park, Hong-Seog; Ahn, Hee-Young; Yoon, Sun-Young; Han, Yoonsoo; Kim, Sangsoo; ***Kim, Jeong-Min*** ; Byun, Sang-Soon; Noh, Seung-Moo; Song, Kyu-Sang; Yoo, Hyang Sook</p>				
IT	<p>Gene, animal RL: DGN (Diagnostic use); PRP (Properties); BIOL (Biological study); USES (Uses) (***HSPA8*** , in diagnosis of gastric cancer; ESTs identifying marker genes for diagnosis of gastric cancer and metastatic gastric cancer)</p>				
IT	<p>Gene, animal RL: DGN (Diagnostic use); PRP (Properties); BIOL (Biological study); USES (Uses) (***HSPB1*** , in diagnosis of gastric cancer; ESTs identifying marker genes for diagnosis of gastric cancer and metastatic gastric cancer)</p>				
IT	<p>Gene, animal RL: DGN (Diagnostic use); PRP (Properties); BIOL (Biological study); USES (Uses) (***HSPCA*** , in diagnosis of gastric cancer; ESTs identifying marker genes for diagnosis of gastric cancer and metastatic gastric cancer)</p>				
IT	<p>Gene, animal</p>				

RL: DGN (Diagnostic use); PRP (Properties); BIOL (Biological study); USES (Uses)
 (***HSPCB*** , in diagnosis of gastric cancer; ESTs identifying marker genes for diagnosis of gastric cancer and metastatic gastric cancer)

L6 ANSWER 4 OF 5 CAPLUS COPYRIGHT 2009 ACS on STN DUPLICATE 2
 AN 2004:485515 CAPLUS <<LOGINID:20090617>>
 DN 141:2160
 TI Gene cataloging and expression profiling in human gastric cancer cells by expressed sequence tags

AU Kim, Nam-Soon; Hahn, Yoonsoo; Oh, Jung-Hwa; Lee, Ju-Yeon; Oh, Kyung-Jin; ***Kim, Jeong-Min*** ; Park, Hong-Seog; Kim, Sangsoo; Song, Kyu-Sang; Rho, Seung-Moo; Yoo, Hyang-Sook; Kim, Yong Sung

CS Laboratory of Human Genomics, Korea Research Institute of Bioscience and Biotechnology, Daejeon, 305-333, S. Korea

SO Genomics (2004), 83(6), 1024-1045
 CODEN: GNMCEP; ISSN: 0888-7543

PB Elsevier Science
 DT Journal
 LA English

AB To understand the mol. mechanism assocd. with gastric carcinogenesis, genes expressed in gastric cancer cell lines and tissues were identified. Of 97,609 high-quality ESTs sequenced from 36 cDNA libraries, 92,545 were coalesced into 10,418 human Unigene clusters (Build 151). The gene expression profile was produced by counting the cluster frequencies in each library. Although the profiles of highly expressed genes varied greatly from library to library, those genes related to cell structure formation, heat shock proteins, the glycolysis pathway, and the signaling pathway were highly represented in human gastric cancer cell lines and in primary tumors. Conversely, the genes encoding Igs, ribosomal proteins, and digestive proteins were down-regulated in gastric cancer cell lines and tissues compared to normal tissues. The transcription levels of some of these genes were confirmed by RT-PCR. Genes related to cell adhesion, apoptosis, and cytoskeleton formation were particularly up-regulated in the gastric cancer cell lines established from malignant ascites compared to those from primary tumors. This comprehensive mol. profiling of human gastric cancer should be useful for elucidating the genetic events assocd. with human gastric cancer. [This abstr. record is one of 24 records for this document necessitated by the large no. of index entries required to fully index the document and publication system constraints.].

AU Kim, Nam-Soon; Hahn, Yoonsoo; Oh, Jung-Hwa; Lee, Ju-Yeon; Oh, Kyung-Jin; ***Kim, Jeong-Min*** ; Park, Hong-Seog; Kim, Sangsoo; Song, Kyu-Sang; Rho, Seung-Moo; Yoo, Hyang-Sook; Kim, Yong Sung

IT Heat-shock proteins
 RL: BSU (Biological study, unclassified); BIOL (Biological study)
 (***HSP*** 27, protein 1; gene cataloging and expression profiling in human gastric cancer cells by expressed sequence tags)

IT Heat-shock proteins
 RL: BSU (Biological study, unclassified); BIOL (Biological study)
 (***HSP*** 70, protein 8; gene cataloging and expression profiling in human gastric cancer cells by expressed sequence tags)

IT Heat-shock proteins
 RL: BSU (Biological study, unclassified); BIOL (Biological study)
 (***HSP*** 90; gene cataloging and expression profiling in human gastric cancer cells by expressed sequence tags)

L6 ANSWER 5 OF 5 CAPLUS COPYRIGHT 2009 ACS on STN

AN 2003:591378 CAPLUS <<LOGINID:20090617>>

DN 139:146183

TI Primers for amplifying mycobacterial heat shock protein ***HSP*** 65
gene and use for identifying mycobacterial species

IN Kim, Bum-joon; Kook, Yoon-ho; ***Kim, Jeong-mi***

PA Biomedlab Corporation, S. Korea

SO PCT Int. Appl., 102 pp.

CODEN: PIXXD2

DT Patent

LA English

FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE				
PI	WO 2003062470	A1	20030731	WO 2003-KR131	20030121				
	W:	AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW							
	RW:	GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG							
	KR 2003063935	A	20030731	KR 2002-4297	20020124				
	KR 2003072087	A	20030913	KR 2002-11648	20020305				
	US 20050014157	A1	20050120	US 2004-500586	20040909				
PRAI	KR 2002-4297	A	20020124						
	KR 2002-11648	A	20020305						
	WO 2003-KR131	W	20030121						
AB	The present invention relates to a pair of primers specific to mycobacterial species, a polynucleotide of an ***HSP*** 65 gene fragment, and a method for the identification of mycobacterial species by using the same. More specifically, the 604-bp ***HSP*** 65 gene fragment can be applied to identification methods of mycobacteria such as the comparative sequence anal. method, the probe hybridization method, and PCR-RFLP, which can resolve the problems of a conventional identification method based on biochem. characteristics, where the genus mycobacterium covers various species and has a low growth rate, and of the problems of 16s rDNA. Thus, according to the identification method of the present invention, the mycobacterial species can be identified simply, economically, and accurately.								
RE.CNT	5	THERE ARE 5 CITED REFERENCES AVAILABLE FOR THIS RECORD							
	ALL CITATIONS AVAILABLE IN THE RE FORMAT								
TI	Primers for amplifying mycobacterial heat shock protein ***HSP*** 65 gene and use for identifying mycobacterial species								
IN	Kim, Bum-joon; Kook, Yoon-ho; ***Kim, Jeong-mi***								
AB	The present invention relates to a pair of primers specific to mycobacterial species, a polynucleotide of an ***HSP*** 65 gene fragment, and a method for the identification of mycobacterial species by using the same. More specifically, the 604-bp ***HSP*** 65 gene fragment can be applied to identification methods of mycobacteria such as the comparative sequence anal. method, the probe. . .								
ST	primer mycobacteria heat shock protein ***hs65*** gene								
IT	Nucleic acid amplification (method)								
	(DNA; primers for amplifying mycobacterial heat shock protein								

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***HSP*** 65 gene and use for identifying mycobacterial species)
IT Heat-shock proteins
RL: ARG (Analytical reagent use); BPN (Biosynthetic preparation); BSU
(Biological study, unclassified); DGN (Diagnostic use); PRP (Properties);
ANST (Analytical study); BIOL (Biological study); PREP (Preparation); USES
(Uses)
( ***HSP*** 65; primers for amplifying mycobacterial heat shock
protein ***HSP*** 65 gene and use for identifying mycobacterial
species)
IT Gene, microbial
RL: ARG (Analytical reagent use); BSU (Biological study, unclassified);
DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL
(Biological study); USES (Uses)
( ***HSP*** 65; primers for amplifying mycobacterial heat shock
protein ***HSP*** 65 gene and use for identifying mycobacterial
species)
IT Diagnosis
(mol.; primers for amplifying mycobacterial heat shock protein
***HSP*** 65 gene and use for identifying mycobacterial species)
IT DNA sequences
Mycobacterium
Mycobacterium BCG
Mycobacterium abscessus
Mycobacterium africanum
Mycobacterium aichiense
Mycobacterium asiaticum
Mycobacterium avium
Mycobacterium avium paratuberculosis
Mycobacterium bovis
Mycobacterium celatum
Mycobacterium chelonae
Mycobacterium chitae
Mycobacterium farcinogenes
Mycobacterium flavescens
Mycobacterium fortuitum
Mycobacterium gastri
Mycobacterium genavense
Mycobacterium gordonae
Mycobacterium haemophilum
Mycobacterium interjectum
Mycobacterium intracellulare
Mycobacterium kansasii
Mycobacterium leprae
Mycobacterium malmoense
Mycobacterium marinum
Mycobacterium microti
Mycobacterium mucogenicum
Mycobacterium neoaurum
Mycobacterium nonchromogenicum
Mycobacterium parafortuitum
Mycobacterium peregrinum
Mycobacterium phlei
Mycobacterium scrofulaceum
Mycobacterium senegalense
Mycobacterium shimoidei
Mycobacterium simiae
Mycobacterium smegmatis

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Mycobacterium szulgai
 Mycobacterium terrae
 Mycobacterium thermoresistibile
 Mycobacterium triviale
 Mycobacterium tuberculosis
 Mycobacterium ulcerans
 Mycobacterium vaccae
 Mycobacterium wolinskyi
 Nocardia carnea
 RFLP (restriction fragment length polymorphism)
 Tsukamurella paurometabola
 Tsukamurella pulmonis
 Tsukamurella tyrosinosolvens
 (primers for amplifying mycobacterial heat shock protein ***HSP***
 65 gene and use for identifying mycobacterial species)

II Primers (nucleic acid)
 RI: ARG (Analytical reagent use); BPN (Biosynthetic preparation); BSU
 (Biological study, unclassified); DGN (Diagnostic use); PRP (Properties);
 ANST (Analytical study); BIOL (Biological study); PREP (Preparation); USES
 (Uses)
 (primers for amplifying mycobacterial heat shock protein ***HSP***
 65 gene and use for identifying mycobacterial species)

IT 569430-56-4 569432-08-2 569432-09-3 569432-10-6 569432-11-7
 569432-12-8 569432-13-9 569432-14-0 569432-15-1 569432-16-2
 569432-17-3 569432-18-4 569432-19-5 569432-20-8 569432-21-9
 569432-22-0 569432-23-1 569432-24-2 569432-25-3 569432-26-4
 569432-27-5 569432-28-6 569432-29-7 569432-30-0 569432-31-1
 569432-32-2 569432-33-3 569432-34-4 569432-35-5 569432-36-6
 569432-37-7 569432-38-8 569432-39-9 569432-40-2 569432-41-3
 569432-42-4 569432-43-5 569432-44-6 569432-45-7 569432-46-8
 569432-47-9 569432-48-0 569432-49-1 569432-50-4 569432-51-5
 569432-52-6 569432-53-7 569432-54-8 569432-55-9
 RI: ARG (Analytical reagent use); BSU (Biological study, unclassified);
 DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL
 (Biological study); USES (Uses)
 (nucleotide sequence; primers for amplifying mycobacterial heat shock
 protein ***HSP*** 65 gene and use for identifying mycobacterial
 species)

IT 569432-56-0
 RI: ARG (Analytical reagent use); BSU (Biological study, unclassified);
 DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL
 (Biological study); USES (Uses)
 (primer ***HSPF3*** sequence; primers for amplifying mycobacterial
 heat shock protein ***HSP*** 65 gene and use for identifying
 mycobacterial species)

IT 569432-57-1
 RI: ARG (Analytical reagent use); BSU (Biological study, unclassified);
 DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL
 (Biological study); USES (Uses)
 (primer ***HSPR3*** sequence; primers for amplifying mycobacterial
 heat shock protein ***HSP*** 65 gene and use for identifying
 mycobacterial species)

IT 81295-43-4, Nuclease, restriction endodeoxyribo-, Xho I
 RI: BUU (Biological use, unclassified); BIOL (Biological study); USES
 (Uses)
 (primers for amplifying mycobacterial heat shock protein ***HSP***
 65 gene and use for identifying mycobacterial species)

IT 569477-29-8
 RL: PRP (Properties)
 (unclaimed sequence; primers for amplifying mycobacterial heat shock
 protein ***HSP*** 65 gene and use for identifying mycobacterial
 species)

=> s hsp65 and primer?
 L7 173 HSP65 AND PRIMER?

=> dup rem 17
 PROCESSING COMPLETED FOR L7
 L8 93 DUP REM L7 (80 DUPLICATES REMOVED)

=> s 18 and (diagnos? or identif?) and mycobact?
 L9 71 L8 AND (DIAGNOS? OR IDENTIF?) AND MYCOBACT?

=> d bib ab kwic 1-
 YOU HAVE REQUESTED DATA FROM 71 ANSWERS - CONTINUE? Y/(N):y

L9 ANSWER 1 OF 71 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN
 AN 2009:116848 BIOSIS <<LOGINID:20090617>>
 DN PREV200900116848
 TI Multi-Probe Real-Time PCR ***Identification*** of Common
 Mycobacterium Species in Blood Culture Broth.
 AU Foongladda, Suporn [Reprint Author]; Pholwat, Suporn; Eampokalap,
 Boonchuay; Kiratisin, Pattarachai; Suthent, Ruengpung
 CS Mahidol Univ, Fac Med, Siriraj Hosp, Dept Microbiol, 2 Prannok Rd, Bangkok
 10700, Thailand
 sisfm@mahidol.ac.th
 SO Journal of Molecular Diagnostics, (JAN 2009) Vol. 11, No. 1, pp. 42-48.
 ISSN: 1525-1578.
 DT Article
 LA English
 ED Entered STN: 11 Feb 2009
 Last Updated on STN: 11 Feb 2009

AB ***Mycobacterium*** tuberculosis complex, *M. avium*, and *M.*
 intracellular are the most common causes of systemic bacterial infection
 in AIDS patients. To ***identify*** these ***mycobacterial***
 isolates in primary blood culture broths, we developed a multiple
 hybridization probe-based real-time PCR assay using the LightCycler
 system. The ***primers*** were designed to amplify a 320-bp fragment
 of ***Mycobacterium*** 16S rRNA genes. Reaction specificity was
 evaluated using PCR amplification curves along with specific melting
 temperatures of probes on DNA extracted from 13 ***Mycobacterium***
 species. In this study, results showed 100% accuracy for the selected
 bacterial panel. Detection limits were 350, 600, and 650 colony-forming
 unit (CFU)/ml blood culture broths for *M. tuberculosis* complex, *M. avium*,
 and *M. intracellular*, respectively (1 to 2 CFU/reaction). To evaluate
 clinical applicability, 341 acid-fast bacilli in blood culture broths were
 analyzed. In total, 327 (96%) were positively ***identified*** : 54.5%
M. tuberculosis complex, 37.5% *M. avium*, and 3.8% *M. intracellular*.
 Results can be available within 3 hours of receiving a broth sample, which
 makes this rapid and simple assay an attractive ***diagnostic*** tool
 for clinical use. (J Mol Diagn 2009, 11:42-48; DOI:
 10.2353/jmoldx.2009.080081)

TI Multi-Probe Real-Time PCR ***Identification*** of Common
 Mycobacterium Species in Blood Culture Broth.

AB ***Mycobacterium*** tuberculosis complex, *M. avium*, and *M.*
 intracellular are the most common causes of systemic bacterial infection
 in AIDS patients. To ***identify*** these ***mycobacterial***
 isolates in primary blood culture broths, we developed a multiple
 hybridization probe-based real-time PCR assay using the LightCycler
 system. The ***primers*** were designed to amplify a 320-bp fragment
 of ***Mycobacterium*** 16S rRNA genes. Reaction specificity was
 evaluated using PCR amplification curves along with specific melting
 temperatures of probes on DNA extracted from 13 ***Mycobacterium***
 species. In this study, results showed 100% accuracy for the selected
 bacterial panel. Detection limits were 350, 600, and 650. . .
 CFU/reaction). To evaluate clinical applicability, 341 acid-fast bacilli
 in blood culture broths were analyzed. in total, 327 (96%) were positively
 identified : 54.5% *M. tuberculosis* complex, 37.5% *M. avium*, and
 3.8% *M. intracellular*. Results can be available within 3 hours of
 receiving a broth sample, which makes this rapid and simple assay an
 attractive ***diagnostic*** tool for clinical use. (J Mol Diagn 2009,
 11:42-48; DOI: 10.2353/jmoldx.2009.080081)

IT Major Concepts
 Infection; Methods and Techniques; Molecular Genetics (Biochemistry and
 Molecular Biophysics)

IT Diseases
 mycobacterial infection: bacterial disease
 Mycobacterium Infections (MeSH)

IT Chemicals & Biochemicals
 16S rRNA gene; blood culture broth

ORGN . . .
 Primates; Mammalia; Vertebrata; Chordata; Animalia
 Organism Name
 human (common): host
 Taxa Notes
 Animals, Chordates, Humans, Mammals, Primates, Vertebrates

ORGN Classifier
 Mycobacteriaceae 08881
 Super Taxa
 Mycobacteria ; Actinomycetes and Related Organisms;
 Eubacteria; Bacteria; Microorganisms
 Organism Name
 Mycobacterium tuberculosis (species): pathogen
 Mycobacterium avium (species): pathogen
 Mycobacterium intracellular (species): pathogen
 Taxa Notes
 Bacteria, Eubacteria, Microorganisms

GEN ***Mycobacterium*** tuberculosis ***hsp65*** gene (
 Mycobacteriaceae)

L9 ANSWER 2 OF 71 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN
 AN 2009:80424 BIOSIS <<LOGINID:20090617>>
 DN PREV200900080424
 TI rpoB sequence-based ***identification*** of ***Mycobacterium***
 avium complex species.

AU Ben Salah, Iskandar; Adekambi, Toidi; Raoult, Didier; Drancourt, Michel
 [Reprint Author]

CS Univ Aix Marseille 2, Fac Med, Unite Rech Malad Infect and Trop Emergentes,
 IFR 48, UMR 6236, CNRS IRD, Marseille, France

Michel.Dfancourt@medecine.univ-mrs.fr
SO Microbiology (Reading), (DEC 2008) Vol. 154, No. Part 12, pp. 3715-3723.
ISSN: 1350-0872.
DT Article
LA English
ED Entered STN: 22 Jan 2009
Last Updated on STN: 22 Jan 2009
AB The ***Mycobacterium*** avium complex (MAC) comprises slowly growing
mycobacteria responsible for opportunistic infections and
zoonoses. The ability to speciate MAC isolates in the clinical
microbiology laboratory is critical for determining the organism
implicated in clinical disease and for epidemiological investigation of
the source of infection. Investigation of a 711 bp variable fragment of
rpoB flanked by the Myco-F/Myco-R ***primers*** found a 0.7-5.1%
divergence among MAC reference strains, with ***Mycobacterium***
chimaera and ***Mycobacterium*** intracellulare being the most closely
related. Using a 0.7 % divergence cut-off, 83% of 100 clinical isolates,
which had been previously ***identified*** by phenotypic
characteristics and 16S-23S rDNA intergenic spacer (ITS) probing, were
identified as M. avium, 8% as M. intracellulare and 2% as M.
chimaera. The uniqueness of seven isolates, exhibiting < 99.3 % rpoB
sequence similarity with MAC reference strains, was confirmed by 16S rDNA,
ITS and ***hsp65*** sequencing and phylogenetic analyses. Partial
rpoB gene sequencing using the Myco-F/Myco-R ***primers*** permits
one-step ***identification*** of MAC isolates at the species level and
the detection of potentially novel MAC species.
TI rpoB sequence-based ***identification*** of ***Mycobacterium***
avium complex species.
AB The ***Mycobacterium*** avium complex (MAC) comprises slowly growing
mycobacteria responsible for opportunistic infections and
zoonoses. The ability to speciate MAC isolates in the clinical
microbiology laboratory is critical for. . . epidemiological
investigation of the source of infection. Investigation of a 711 bp
variable fragment of rpoB flanked by the Myco-F/Myco-R ***primers***
found a 0.7-5.1% divergence among MAC reference strains, with
Mycobacterium chimaera and ***Mycobacterium*** intracellulare
being the most closely related. Using a 0.7 % divergence cut-off, 83% of
100 clinical isolates, which had been previously ***identified*** by
phenotypic characteristics and 16S-23S rDNA intergenic spacer (ITS)
probing, were ***identified*** as M. avium, 8% as M. intracellulare
and 2% as M. chimaera. The uniqueness of seven isolates, exhibiting <
99.3 % rpoB sequence similarity with MAC reference strains, was confirmed
by 16S rDNA, ITS and ***hsp65*** sequencing and phylogenetic analyses.
Partial rpoB gene sequencing using the Myco-F/Myco-R ***primers***
permits one-step ***identification*** of MAC isolates at the species
level and the detection of potentially novel MAC species.
IT . . .
and Molecular Biophysics)
IT Diseases
infection: infectious disease
Infection (MeSH)
IT Chemicals & Biochemicals
rpoB; 16S-23S rDNA: intergenic spacer probing; Myco-F ***primer*** ;
Myco-R ***primer***
ORGN Classifier
Mycobacteriaceae 08881
Super Taxa

Mycobacteria ; Actinomycetes and Related Organisms;
 Eubacteria; Bacteria; Microorganisms
 Organism Name
 Mycobacterium avium (species): pathogen
 Mycobacterium intracellulare (species): pathogen
 Mycobacterium avium complex (species): pathogen
 Mycobacterium chimaera (species): pathogen
 Taxa Notes
 Bacteria, Eubacteria, Microorganisms
 GEN ***Mycobacterium*** avium complex rpoB gene (***Mycobacteriaceae***
)
 L9 ANSWER 3 OF 71 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN
 AN 2008:704929 BIOSIS <<LOGINID::20090617>>
 DN PREV200800704928
 TI ***Identification*** of individual DNA molecule of
 Mycobacterium tuberculosis by nested PCR-RFLP and capillary
 electrophoresis.
 AU Chang, Po-Ling; Hsieh, Wen-Shyang; Chiang, Chia-Lien; Yen-Liberman,
 Belinda; Procop, Gary W.; Chang, Huan-Tsung [Reprint Author]; Ho,
 Hsin-Tsung
 CS Natl Taiwan Univ, Dept Chem, Taipei 10764, Taiwan
 changht@ntu.edu.tw; drho@ms2.mmh.org.tw
 SO Talanta, (OCT 15 2008) Vol. 77, No. 1, pp. 182-188.
 CODEN: TLNTA2. ISSN: 0039-9140.
 DT Article
 LA English
 ED Entered STN: 3 Dec 2008
 Last Updated on STN: 3 Dec 2008
 AB The improvement of sensitivity and differentiation in rapidly
 identifying a small amount of ***mycobacteria*** in sputum
 has
 significant implications for reducing tuberculosis transmission. We
 previously applied the conventional PCR and capillary electrophoresis (CE)
 to establish the restriction fragment length polymorphism (RFLP) pattern
 of ***mycobacterial*** 65-kDa heat shock protein (***hsp65***)
 gene from colony specimens. However, the previous analysis did not
 provide enough sensitivity for sputum specimens in which the limitation of
 analysis might be hindered by PCR inhibitors and ***primer*** -dimers
 formation during amplification. In the current study, nested PCR (nPCR)
 had been redesigned for PCR-RFLP analysis (PRA) of ***mycobacterial***
 hsp65 gene using CE. The results show both ***Mycobacterium***
 tuberculosis complex and ***mycobacteria*** other than tuberculosis
 could be ***identified*** in the presence of PCR inhibitors. The
 interference due to ***primer*** -dimers was also minimized. Based on
 the Poisson distribution, the repeatability of single DNA molecule
 detection was greatly affected by sampling probability and might be
 improved significantly by increasing the sample loading. The PRA using
 nPCR and CE is not only able to detect the individual
 mycobacterial DNA molecule but also potentially differentiate the
 species. (c) 2008 Elsevier B.V. All rights reserved.
 TI ***Identification*** of individual DNA molecule of
 Mycobacterium tuberculosis by nested PCR-RFLP and capillary
 electrophoresis.
 AB The improvement of sensitivity and differentiation in rapidly
 identifying a small amount of ***mycobacteria*** in sputum
 has

significant implications for reducing tuberculosis transmission. We previously applied the conventional PCR and capillary electrophoresis (CE) to establish the restriction fragment length polymorphism (RFLP) pattern of ***mycobacterial*** 65-kDa heat shock protein (***hsp65***) gene from colony specimens. However, the previous analysis did not provide enough sensitivity for sputum specimens in which the limitation of analysis might be hindered by PCR inhibitors and ***primer*** -dimers formation during amplification. In the current study, nested PCR (nPCR) had been redesigned for PCR-RFLP analysis (PRA) of ***mycobacterial*** ***hsp65*** gene using CE. The results show both ***Mycobacterium*** tuberculosis complex and ***mycobacteria*** other than tuberculosis could be ***identified*** in the presence of PCR inhibitors. The interference due to ***primer*** -dimers was also minimized. Based on the Poisson distribution, the repeatability of single DNA molecule detection was greatly affected by sampling. . . significantly by increasing the sample loading. The PRA using nPCR and CE is not only able to detect the individual ***mycobacterial*** DNA molecule but also potentially differentiate the species. (c) 2008 Elsevier B.V. All rights reserved.

IT . . .
Structures, & Systems of Organisms
sputum
IT Diseases
tuberculosis: bacterial disease, transmission
Tuberculosis (MeSH)
IT Chemicals & Biochemicals
PCR inhibitor; DNA: ***identification*** ; ***primer*** -dimer:
formation
ORGN Classifier
Mycobacteriaceae 08881
Super Taxa
Mycobacteria ; Actinomycetes and Related Organisms;
Eubacteria; Bacteria; Microorganisms
Organism Name
Mycobacterium tuberculosis (species)
Taxa Notes
Bacteria, Eubacteria, Microorganisms
GEN ***Mycobacterium*** tuberculosis ***hsp65*** gene [
Mycobacterium tuberculosis 65-kDa heat shock protein gene] (
Mycobacteriaceae)
L9 ANSWER 4 OF 71 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN
AN 2008:586534 BIOSIS <<LOGINID:20090617>>
DN PREV200800586533
TI ***Mycobacterium*** porcinum strains isolated from bovine bulk milk:
Implications for ***Mycobacterium*** avium subsp paratuberculosis
detection by PCR and culture.
AU Taddei, R. [Reprint Author]; Barbieri, I.; Pacciarini, M. L.; Fallacara,
F.; Belletti, G. L.; Arrigoni, N.
CS Ist Zooprofilattico Sperimentale Lombardia and Emil, Sez Forli, Via
Marchini 1, I-47100 Forli, Italy
roberta.taddei@bs.izs.it
SO Veterinary Microbiology, (AUG 25 2008) Vol. 130, No. 3-4, pp. 338-347.
CODEN: VMICDQ. ISSN: 0378-1135.
DT Article
LA English
ED Entered STN: 22 Oct 2008

Last Updated on STN: 22 Oct 2008

AB In this study, the isolation of 52 ***mycobactin*** -independent fast growing ***mycobacteria*** from 631 bulk milk samples (8.2%), is reported. These strains, isolated during a bulk milk survey for ***Mycobacterium*** avium subsp. paratuberculosis (Map), strongly affected Map detection both by PCR and by culture, as they gave a positive IS900 PCR signal and resulted to totally inhibit the growth of Map when spotted on HEYM slants already inoculated with 200 μ l of 10-fold dilutions containing from 5 x 10 to 5 x 10³ Map cells/ml. 16S rDNA gene sequencing, using the MicroSeq 500 16S rDNA Bacterial Sequencing Kit (Applied Biosystems), was performed on a subset of six strains, ***identifying*** ***Mycobacterium*** porcinum with 100% homology in all six cases. The 52 strains were characterized by PCR-restriction fragment length polymorphism (RFLP) analysis of the ***hsp65*** gene, which confirmed the ***identification*** of M. porcinum for all the isolates. Using specific ***primers*** designed on the Map-IS900 sequence and on the M. porcinum sequence determined in this study, a 1385 bp sequence from the M. porcinum genome was characterized. This IS900-like sequence showed 82% homology with Map IS900. From our findings the following results emerged: (a) any culture showing one or more M. porcinum colonies represents a potential "false negative" result and should therefore be considered as contaminated; (b) IS900-like elements could be more widespread than was previously thought; (c) IS900 PCR positive results should be interpreted cautiously, as confirmed by the evidence that the ***primer*** pair used in this study resulted not to be specific (C) 2008 Elsevier B.V. All rights reserved.

TI ***Mycobacterium*** porcinum strains isolated from bovine bulk milk: Implications for ***Mycobacterium*** avium subsp paratuberculosis detection by PCR and culture.

AB In this study, the isolation of 52 ***mycobactin*** -independent fast growing ***mycobacteria*** from 631 bulk milk samples (8.2%), is reported. These strains, isolated during a bulk milk survey for ***Mycobacterium*** avium subsp. paratuberculosis (Map), strongly affected Map detection both by PCR and by culture, as they gave a positive IS900. . . sequencing, using the MicroSeq 500 16S rDNA Bacterial Sequencing Kit (Applied Biosystems), was performed on a subset of six strains, ***identifying*** ***Mycobacterium*** porcinum with 100% homology in all six cases. The 52 strains were characterized by PCR-restriction fragment length polymorphism (RFLP) analysis of the ***hsp65*** gene, which confirmed the ***identification*** of M. porcinum for all the isolates. Using specific ***primers*** designed on the Map-IS900 sequence and on the M. porcinum sequence determined in this study, a 1385 bp sequence from. . . than was previously thought; (c) IS900 PCR positive results should be interpreted cautiously, as confirmed by the evidence that the ***primer*** pair used in this study resulted not to be specific (C) 2008 Elsevier B.V. All rights reserved.

ORGN . . .
 Chordata; Animalia
 Organism Name
 bovine (common): host
 Taxa Notes
 Animals, Artiodactyls, Chordates, Mammals, Nonhuman Vertebrates,
 Nonhuman Mammals, Vertebrates

ORGN Classifier
 Mycobacteriaceae 08881

Super Taxa

Mycobacteria ; Actinomycetes and Related Organisms;
Eubacteria; Bacteria; Microorganisms
Organism Name
Mycobacterium avium paratuberculosis (subspecies): pathogen
Mycobacterium porcinum (species): pathogen
Taxa Notes
Bacteria, Eubacteria, Microorganisms

L9 ANSWER 5 OF 71 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN
AN 2007:529420 BIOSIS <<LOGINID:20090617>>
DN PREV200700528890

TI ***Mycobacterium*** species ***identification*** - A new approach
via dnaJ gene sequencing.

AU Yamada-Noda, Makiko; Ohkusu, Kiyofumi; Hata, Hiroyuki; Shah, Mohammad
Monir; Nhung, Pham Hong; Sun, Xiao Song; Hayashi, Masahiro; Ezaki,
Takayuki [Reprint Author]

CS Gifu Univ, Grad Sch Med, Dept Microbiol Regenerat and Adv Med Sci, 1-1
Yanagido, Gifu 5011194, Japan
tezaki@gifu-u.ac.jp

SO Systematic and Applied Microbiology, (SEP 2007) Vol. 30, No. 6, pp.
453-462.

CODEN: SAMIDF. ISSN: 0723-2020.

DT Article

LA English

ED Entered STN: 10 Oct 2007

Last Updated on STN: 10 Oct 2007

AB The availability of the dnaJ gene for ***identifying***

Mycobacterium species was examined by analyzing the complete
dnaJ1

sequences (approximately 1200 bp) of 56 species (54 of them were type
strains) and comparing sequence homologies with those of the 16S rRNA gene
and other housekeeping genes (rpoB, ***hsp65***). Among the 56

Mycobacterium species, the mean sequence similarity of the dnaJ1
gene (80.4%) was significantly less than that of the 16S rRNA, rpoB and
hsp65 genes (96.6 %, 91.3 % and 9 1.1 %, respectively),

indicating

a high discriminatory power of the dnaJ1 gene. Seventy-one clinical
isolates were correctly clustered to the corresponding type strains,
showing isolates belonging to the same species. In order to propose a
method for strain ***identification***, we ***identified*** an
area with a high degree of polymorphism, bordered by conserved sequences,
that can be used as universal ***primers*** for PCR amplification and
sequencing. The sequence of this fragment (approximately 350bp) allows
accurate species ***identification*** and may be used as a new tool
for the ***identification*** of ***Mycobacterium*** species. (c)
2007 Published by Elsevier GmbH.

TI ***Mycobacterium*** species ***identification*** - A new approach
via dnaJ gene sequencing.

AB The availability of the dnaJ gene for ***identifying***

Mycobacterium species was examined by analyzing the complete
dnaJ1

sequences (approximately 1200 bp) of 56 species (54 of them were type
strains) and comparing sequence homologies with those of the 16S rRNA gene
and other housekeeping genes (rpoB, ***hsp65***). Among the 56

Mycobacterium species, the mean sequence similarity of the dnaJ1
gene (80.4%) was significantly less than that of the 16S rRNA, rpoB and

hsp65 genes (96.6 %, 91.3 % and 9 1.1 %, respectively), indicating a high discriminatory power of the dnaJ gene. Seventy-one. . . to the corresponding type strains, showing isolates belonging to the same species. In order to propose a method for strain ***identification***, we ***identified*** an area with a high degree of polymorphism, bordered by conserved sequences, that can be used as universal ***primers*** for PCR amplification and sequencing. The sequence of this fragment (approximately 350bp) allows accurate species ***identification*** and may be used as a new tool for the ***identification*** of ***Mycobacterium*** species. (c) 2007 Published by Elsevier GmbH.

ORGN Classifier

Mycobacteriaceae 08881

Super Taxa

Mycobacteria ; Actinomycetes and Related Organisms;

Eubacteria; Bacteria; Microorganisms

Organism Name

Mycobacterium tuberculosis (species)
 Mycobacterium avium (species)
 Mycobacterium kansasii (species)
 Mycobacterium (genus)
 Mycobacterium gastris (species)
 Mycobacterium ulcerans (species)
 Mycobacterium mucogenicum (species)
 Mycobacterium parafortuitum (species)
 Mycobacterium genavense (species)
 Mycobacterium scrofulaceum (species)

Taxa Notes

Bacteria, Eubacteria, Microorganisms

ORGN Classifier

Nocardioform Actinomycetes 08810

Super Taxa

Actinomycetes and Related Organisms; Eubacteria; Bacteria; . . .

GEN ***Mycobacterium*** dnaJ gene (***Mycobacteriaceae***): polymorphism; ***Mycobacterium*** rpoB gene (***Mycobacteriaceae***): polymorphism; ***Mycobacterium*** ***hsp65*** gene (***Mycobacteriaceae***): polymorphism

L9 ANSWER 6 OF 71 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN
 AN 2007:419642 BIOSIS <<LOGINID::20090617>>

DN PREV200700424384

TI Detection of ***Mycobacterium*** species distribution in the sputum samples of tuberculosis patients by PCR-RFLP method in Elazig province. Original Title: ELAZIG YORESINDE TUBERKULOZLU HASTALARIN BALGAM ORNEKLERINDE MIKOBAKTERI TUR DAGILIMININ PCR-RFLP YONTEMI ILE BELIRLENMESI.

AU Agacayak, Ahmet [Reprint Author]; Bulut, Yasemin; Seyrek, Adnan
 CS Firat Univ, Tip Fak, Mikrobiyoloji and Klin Mikrobiyoloji Anabilim Dalı, Elazig, Turkey
 ybulut@firat.edu.tr

SO Mikrobiyoloji Bulteni, (APR 2007) Vol. 41, No. 2, pp. 203-209.
 CODEN: MIBUBI. ISSN: 0374-9096.

DT Article

LA Turkish

ED Entered STN: 8 Aug 2007

Last Updated on STN: 7 Nov 2007

- AB The aim of this study was to detect the ***Mycobacterium*** species in the sputum samples collected from tuberculosis patients in Elazig province (located in Eastern Anatolia, Turkey), by PCR-RFLP (Polymerase Chain Reaction-Restriction Fragment Length Polymorphism) method. A total of 60 samples from patients (32 male, 28 female) who were ***diagnosed*** as tuberculosis by culture positivity at Elazig Tuberculosis Control Dispensary, were included to the study. After DNA extraction and isolation from the samples, gene region encoding for 65 kDa protein of ***mycobacteria*** was amplified with specific ***primers*** (first step ***primers*** : TB1; 5'-GAG ATC GAC TGG AGG ATC C-3' and TB2; 5'-AGC TGC AGC CCA AAG GTG TT- 3', second step ***primers*** : TB1 and TB3; 5'-GTG TTG GAC TCC TCG ACG GT-3') by using seminested PCR method. According to ***hsp65*** gene region amplification, 51 (85%) samples yielded positive results, while nine (15%) samples could not be ***identified***. Of 51 samples, 44 (86.3%) were ***identified*** as M.tuberculosis complex, four (7.8%) were M.scrofulaceum, two (3.9%) were M.avium and one (1.9%) was M.intracellulare, in the restriction assay by HaeIII of the PCR products. In order to ***identify*** the species of M.tuberculosis complex, gyrB gene region was amplified in those of 44 samples with specific ***primers*** (MTUB-f; 5'-TCG GAC GCG TAT GCG ATA TC-3' and MTUB-r; 5'-ACA TAC AGT TCG GAC TTG CG-3'), and the PCR products were restricted by RsaI and TaqI enzymes. In this assay, 34 (77.3%), eight (18.2%), one (2.3%) and one (2.3%) of the 44 M.tuberculosis complex samples were detected as M.tuberculosis, M.bovis, M.microti and M.africanum, respectively. Our data indicated that at least seven different ***Mycobacterium*** species were the causative agents of tuberculosis in our region. As a result, researching for species distributions of ***mycobacteria*** in all of the parts of Turkey by molecular methods and clarifying their resistance patterns against antituberculous drugs are needed for the effective control of tuberculosis.
- TI Detection of ***Mycobacterium*** species distribution in the sputum samples of tuberculosis patients by PCR-RFLP method in Elazig province. Original Title: ELAZIG YORESINDE TUBERKULOZLU. . .
- AB The aim of this study was to detect the ***Mycobacterium*** species in the sputum samples collected from tuberculosis patients in Elazig province (located in Eastern Anatolia, Turkey), by PCR-RFLP (Polymerase Chain Reaction-Restriction Fragment Length Polymorphism) method. A total of 60 samples from patients (32 male, 28 female) who were ***diagnosed*** as tuberculosis by culture positivity at Elazig Tuberculosis Control Dispensary, were included to the study. After DNA extraction and isolation from the samples, gene region encoding for 65 kDa protein of ***mycobacteria*** was amplified with specific ***primers*** (first step ***primers*** : TB1; 5'-GAG ATC GAC TGG AGG ATC C-3' and TB2; 5'-AGC TGC AGC CCA AAG GTG TT- 3', second step ***primers*** : TB1 and TB3; 5'-GTG TTG GAC TCC TCG ACG GT-3') by using seminested PCR method. According to ***hsp65*** gene region amplification, 51 (85%) samples yielded positive results, while nine (15%) samples could not be ***identified***. Of 51 samples, 44 (86.3%) were ***identified*** as M.tuberculosis complex, four (7.8%) were M.scrofulaceum, two (3.9%) were M.avium and one (1.9%) was M.intracellulare, in the restriction assay by HaeIII of the PCR products. In order to ***identify*** the species of M.tuberculosis complex, gyrB gene region was amplified in those of 44 samples with specific ***primers*** (MTUB-f; 5'-TCG GAC GCG TAT GCG ATA TC-3' and MTUB-r; 5'-ACA TAC AGT TCG GAC TTG CG-3'), and the PCR. . M.tuberculosis complex samples were detected as M.tuberculosis, M.bovis, M.microti and M.africanum, respectively. Our data indicated that

at least seven different ***Mycobacterium*** species were the causative agents of tuberculosis in our region. As a result, researching for species distributions of ***mycobacteria*** in all of the parts of Turkey by molecular methods and clarifying their resistance patterns against antituberculous drugs are needed. . .

IT . . .
 (Biochemistry and Molecular Biophysics)

IT Parts, Structures, & Systems of Organisms
 sputum

IT Diseases
 tuberculosis: bacterial disease, infectious disease, epidemiology,
 ****diagnosis***
 Tuberculosis (MeSH)

IT Chemicals & Biochemicals
 DNA

ORGN . . .
 Vertebrata; Chordata; Animalia
 Organism Name
 human (common): host, female, male
 Taxa Notes
 Animals, Chordates, Humans, Mammals, Primates, Vertebrates

ORGN Classifier
 Mycobacteriaceae 08881
 Super Taxa
 Mycobacteria ; Actinomycetes and Related Organisms;
 Eubacteria; Bacteria; Microorganisms
 Organism Name
 Mycobacterium tuberculosis (species): pathogen
 Mycobacterium bovis (species): pathogen
 Mycobacterium avium (species): pathogen
 Mycobacterium intracellulare (species): pathogen
 Mycobacterium scrofulaceum (species): pathogen
 Mycobacterium microti (species): pathogen
 Mycobacterium africanum (species): pathogen
 Taxa Notes
 Bacteria, Eubacteria, Microorganisms

L9 ANSWER 7 OF 71 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN
 AN 2007:36655 BIOSIS <<LOGINID:20090617>>
 DN PREV200700037125
 TI Study of PCR for direct detection and ***identification*** of
 mycobacteria in skin specimens.

AU Wang Hong-sheng [Reprint Author]; Li Xiao-jie; Wu Qin-xue; Cui Pan-gen;
 Liu Xun-quan

CS Chinese Acad Med Sci, Inst Dermatol, Nanjing 210042, Peoples R China
 wuqx2003@hotmail.com

SO Zhonghua Pifuke Zazhi, (OCT 2006) Vol. 39, No. 10, pp. 593-595.
 CODEN: CHFTAJ. ISSN: 0412-4030.

DT Article
 LA Chinese
 ED Entered STN: 27 Dec 2006
 Last Updated on STN: 27 Dec 2006

AB Objective To study the possibility of direct detection and
 identification of ***mycobacteria*** by PCR in skin
 specimens. Methods The comparison of PCR with in vitro culture of M.
 smegmatis was conducted at three levels. First, serial dilutions of M.
 smegmatis DNA was amplified with ***primers*** aiming at

hsp65 gene to testify the sensitivity of PCR for
 mycobacterial detection, and the same dilutions of suspension of

M smegmatis was inoculated in Lowenstein-Jensen medium to assessed the sensitivity of in vitro culture. Secondly, the results of detecting simulant clinical specimens by PCR with or without pretreatment were compared with those by in vitro culture. Thirdly, the results of detecting 37 clinical skin specimens suspected to be infected with ***mycobacteria*** by PCR with or without pretreatment were compared with those by in vitro culture. Results The sensitivity of both PCR and in vitro culture for detection of serial dilutions of bacterial suspension of M. smegmatis was $1 \times 10(2)$ cells/mL. The detection rates of PCR for simulant clinical skin specimen at $1 \times 10(2)$ cells/mL with and without pretreatment were 60% and 0 respectively, and the detection rates of in vitro culture were 80% and 100%, respectively. The detection rate of PCR was 100% for simulant clinical skin specimens at $1 \times 10(3)$ cells/mL. From the 37 clinical skin specimens, 7 and 2 positive cases were detected by PCR with and without pretreatment respectively, however, 9 positive cases were detected by in vitro culture. Conclusion With the pretreatment of clinical skin specimens, the sensitivity of PCR approximates 80% and the time needed for detection is obviously shortened.

TI Study of PCR for direct detection and ***identification*** of
 mycobacteria in skin specimens.

AB Objective To study the possibility of direct detection and
 identification of ***mycobacteria*** by PCR in skin specimens. Methods The comparison of PCR with in vitro culture of M smegmatis was conducted at three levels. First, serial dilutions of M. smegmatis DNA was amplified with ***primers*** aiming at
 hsp65 gene to testify the sensitivity of PCR for
 mycobacterial detection, and the same dilutions of suspension of

M smegmatis was inoculated in Lowenstein-Jensen medium to assessed the sensitivity of. . . with those by in vitro culture. Thirdly, the results of detecting 37 clinical skin specimens suspected to be infected with ***mycobacteria*** by PCR with or without pretreatment were compared with those by in vitro culture. Results The sensitivity of both PCR and. . .

ORGN Classifier
 Mycobacteriaceae 08881
 Super Taxa
 Mycobacteria ; Actinomycetes and Related Organisms;
 Eubacteria; Bacteria; Microorganisms
 Organism Name
 Mycobacteria smegmatis (species)
 Taxa Notes
 Bacteria, Eubacteria, Microorganisms

GEN ***Mycobacteria*** smegmatis ***hsp65*** gene (
 Mycobacteriaceae)

L9 ANSWER 8 OF 71 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN
 AN 2006:321383 BIOSIS <LOGINID:20090617>
 DN PREV200600320304
 TI Detection of ***mycobacteria*** in Crohn's disease by a broad spectrum polymerase chain reaction.
 AU Tzen, Chi-Yuan; Wu, Tsu-Yen; Tzen, Chin-Yuan [Reprint Author]
 CS Mackay Mem Hosp, Dept Pathol, 45 Minsheng Rd, Taipei, Taiwan
 jeffrey@ms2.mnh.gov.tw

SO Journal of the Formosan Medical Association, (APR 2006) Vol. 105, No. 4,
pp. 290-298.
ISSN: 0929-6646.

DT Article
LA English
ED Entered STN: 21 Jun 2006
Last Updated on STN: 21 Jun 2006

AB Background: The role of ***mycobacterial*** infection, particularly related to ***Mycobacterium*** avium subsp paratuberculosis (Map), in Crohn's disease has long been debated. We developed ***primer*** pairs capable of detecting a broad spectrum of ***mycobacterium*** and employed them to investigate surgical specimens from patients with Crohn's disease. Methods: Pan ***mycobacterium*** ***primers*** of the 65-kDa heat shock protein gene (***Hsp65***) were used in a polymerase chain reaction (PCR) to examine 12 surgical ly-resected, formalin-fixed, paraffin-embedded specimens from 11 patients with Crohn's disease. The DNA sequences of amplicons were aligned with those in GenBank. Results: ***Mycobacterial*** DNA was found in specimens from three of 11 patients. M. mucogenicum was ***identified*** in a specimen from one patient and M. tuberculosis in two, but Map was not ***identified*** in any. Conclusion: ***Hsp65*** -based PCR can be employed to search for occult ***mycobacterial*** infection of the gastrointestinal tract in patients with a ***diagnosis*** or suspicion of Crohn's disease. This approach may have a therapeutic implication. [J Formos Med Assoc 2006;105(4):290-298].

TI Detection of ***mycobacteria*** in Crohn's disease by a broad spectrum polymerase chain reaction.

AB Background: The role of ***mycobacterial*** infection, particularly related to ***Mycobacterium*** avium subsp paratuberculosis (Map), in Crohn's disease has long been debated. We developed ***primer*** pairs capable of detecting a broad spectrum of ***mycobacterium*** and employed them to investigate surgical specimens from patients with Crohn's disease. Methods: Pan ***mycobacterium*** ***primers*** of the 65-kDa heat shock protein gene (***Hsp65***) were used in a polymerase chain reaction (PCR) to examine 12 surgical ly-resected, formalin-fixed, paraffin-embedded specimens from 11 patients with Crohn's disease. The DNA sequences of amplicons were aligned with those in GenBank. Results: ***Mycobacterial*** DNA was found in specimens from three of 11 patients. M. mucogenicum was ***identified*** in a specimen from one patient and M. tuberculosis in two, but Map was not ***identified*** in any. Conclusion: ***Hsp65*** -based PCR can be employed to search for occult ***mycobacterial*** infection of the gastrointestinal tract in patients with a ***diagnosis*** or suspicion of Crohn's disease. This approach may have a therapeutic implication. [J Formos Med Assoc 2006;105(4):290-298].

ORGN . . .
Organism Name
 human (common): adult, middle age, host, female, male
Taxa Notes
 Animals, Chordates, Humans, Mammals, Primates, Vertebrates

ORGN Classifier
 Mycobacteriaceae 08881
Super Taxa
 Mycobacteria ; Actinomycetes and Related Organisms;
 Eubacteria; Bacteria; Microorganisms
Organism Name
 Mycobacterium tuberculosis (species): pathogen

Mycobacterium avium paratuberculosis (subspecies): pathogen
 Mycobacterium mucogenicum (species)

Taxa Notes

Bacteria, Eubacteria, Microorganisms

GEN ***Mycobacterium*** avium paratuberculosis ***Hsp65*** gene [

Mycobacterium avium paratuberculosis heat shock protein 65 gene]
 (

Mycobacteriaceae)

L9 ANSWER 9 OF 71 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN
 AN 2003:556261 BIOSIS <<LOGINID::20090617>>
 DN PREV200300556972
 TI ***Identification*** of ***Mycobacterium*** species and
 characterization of strains using a labchip (microfluidic) instrument.
 AU Cooksey, R. C. [Reprint Author]; Limor, J. R. [Reprint Author]
 CS CDC, Atlanta, GA, USA
 SO Abstracts of the General Meeting of the American Society for Microbiology,
 (2003) Vol. 103, pp. U-029.
<http://www.asmsa.org/mtgsrvc/generalmeeting.htm>. cd-rom.
 Meeting Info.: 103rd American Society for Microbiology General Meeting.
 Washington, DC, USA. May 18-22, 2003. American Society for Microbiology.
 ISSN: 1060-2011 (ISSN print).
 DT Conference; (Meeting)
 LA Conference; Abstract; (Meeting Abstract)
 ED English
 Entered STN: 26 Nov 2003
 Last Updated on STN: 26 Nov 2003
 AB We developed schemes for rapid ***identification*** of
 Mycobacterium species and strain typing using a labchip
 instrument
 (Agilent Model 2100 Bioanalyzer) which uses electrokinetic forces to drive
 samples through chip microchannels (microfluidics), enabling real-time
 resolution and detection of sample components. A 439-bp region of
 hsp65 that has sequence polymorphisms specific for most
 mycobacterial species has been characterized by PCR restriction
 analysis (PRA) with BstEII or HaeIII as a species ***identification***
 tool. We performed PRA in duplicate, using 2 strains each of 13 species,
 and analyzing 1 ul of each digest. Fragment sizes (bp) determined
 automatically by the instrument were consistently smaller than the correct
 sizes for each of the species as determined by sequence analysis (mean
 variance, 7.5%) but varied by 1 to 6 bp for specific fragments in
 duplicate runs. M. tuberculosis isolates were typed with the labchip
 instrument by using ***mycobacterial*** interspersed repetitive unit
 (MIRU) typing, a variable number tandem repeat typing method which
 determines the number of copies of repeated units at 12 loci scattered
 throughout the genome based on product size after PCR amplification.
 Eleven isolates with 1 to 6 repeat copies at each locus were examined.
 Sizes were smaller by a mean of 4% compared to correct sizes predicted by
 sequence analysis, varied on duplicate runs by 1 to 5 bp, and could be
 used to correctly ***identify*** all strain types. Nontuberculous
 Mycobacterium species were typed using randomly amplified
 polymorphic DNA (RAPD) electrophoresis on the labchip instrument. PCR
 using a single 10-mer ***primer*** and low annealing temperature
 (37degreeC) was performed using 5 clusters each of M. chelonae, M.
 abscessus, and M. mucogenicum (13 isolates of each species) and 3 clusters
 of M. avium (11 isolates). All clusters were distinguished when patterns
 were compared to results of pulsed-field gel electrophoresis. RAPD

patterns for 1 M. abscessus strain were unchanged when we tested DNA from 2 cultures or DNA extracted on 6 different days from the same culture. The labchip instrument is a versatile alternative for sizing ***mycobacterial*** DNA fragments.

TI ***Identification*** of ***Mycobacterium*** species and characterization of strains using a labchip (microfluidic) instrument.

AB We developed schemes for rapid ***identification*** of ***Mycobacterium*** species and strain typing using a labchip instrument (Agilent Model 2100 Bioanalyzer) which uses electrokinetic forces to drive samples through chip microchannels (microfluidics), enabling real-time resolution and detection of sample components. A 439-bp region of ***hsp65*** that has sequence polymorphisms specific for most ***mycobacterial*** species has been characterized by PCR restriction analysis (PRA) with BstEII or HaeIII as a species ***identification*** tool. We performed PRA in duplicate, using 2 strains each of 13 species, and analyzing 1 ul of each digest... by ltoreq6 bp for specific fragments in duplicate runs. M. tuberculosis isolates were typed with the labchip instrument by using ***mycobacterial*** interspersed repetitive unit (MIRU) typing, a variable number tandem repeat typing method which determines the number of copies of repeated... to correct sizes predicted by sequence analysis, varied on duplicate runs by ltoreq5 bp, and could be used to correctly ***identify*** all strain types. Nontuberculous ***Mycobacterium*** species were typed using randomly amplified polymorphic DNA (RAPD) electrophoresis on the labchip instrument. PCR using a single 10-mer ***primer*** and low annealing temperature (37/degreeC) was performed using 5 clusters each of M. chelonae, M. abscessus, and M. mucogenicum (13... or DNA extracted on 6 different days from the same culture. The labchip instrument is a versatile alternative for sizing ***mycobacterial*** DNA fragments.

IT Major Concepts
Equipment Apparatus Devices and Instrumentation; Human Medicine (Medical Sciences); Infection; Methods and Techniques

IT Diseases
mycobacterial infection: bacterial disease
Mycobacterium Infections (MeSH)

IT Chemicals & Biochemicals
DNA: analysis, extraction, fragment sizing

IT Methods & Equipment
PCR [polymerase chain reaction]: genetic techniques, laboratory techniques; labchip (microfluidic) instrument: laboratory equipment; ***mycobacterial*** interspersed repetitive unit typing: clinical techniques, ***diagnostic*** techniques, genetic techniques, laboratory techniques; restriction analysis: genetic techniques, laboratory techniques

IT Miscellaneous Descriptors
annealing temperatures; ***diagnostics*** ; medical bacteriology; methodology

ORGN . . .
Taxa
Primates; Mammalia; Vertebrata; Chordata; Animalia
Organism Name
human (common)
Taxa Notes
Animals, Chordates, Humans, Mammals, Primates, Vertebrates

ORGN Classifier
Mycobacteriaceae 08881

Super Taxa

Mycobacteria ; Actinomycetes and Related Organisms;
 Eubacteria; Bacteria; Microorganisms
 Organism Name
 Mycobacterium abscessus (species): pathogen
 Mycobacterium avium (species): pathogen
 Mycobacterium chelonae (species): pathogen
 Mycobacterium mucogenicum (species): pathogen
 Mycobacterium spp. (species): pathogen, species
 identification methods, strain characterization methods

Taxa Notes

Bacteria, Eubacteria, Microorganisms

L9 ANSWER 10 OF 71 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on
 STN
 AN 2003:518694 BIOSIS <<LOGINID::20090617>>
 DN PREV200300520305
 TI Rapid ***identification*** of ***Mycobacterium*** species by
 hsp65 partial gene sequence.
 AU McNabb, A. [Reprint Author]; Eisler, D. [Reprint Author]; Adie, K.
 [Reprint Author]; Amos, M. [Reprint Author]; Rodrigues, M. [Reprint
 Author]; Isaac-Renton, J. [Reprint Author]
 CS British Columbia Centre for Disease Control, Vancouver, BC, Canada
 SO Abstracts of the General Meeting of the American Society for Microbiology,
 (2003) Vol. 103, pp. C-220.
<http://www.asmsa.org/mtgsrsrc/generalmeeting.htm>. cd-rom.
 Meeting Info.: 103rd American Society for Microbiology General Meeting.
 Washington, DC, USA. May 18-22, 2003. American Society for Microbiology.
 ISSN: 1060-2011 (ISSN print).
 DT Conference; (Meeting)
 Conference; Abstract; (Meeting Abstract)
 LA English
 ED Entered STN: 5 Nov 2003
 Last Updated on STN: 5 Nov 2003
 AB Currently, ***Mycobacterium*** species are ***identified*** using
 biochemical tests, mycolic acid analysis and commercial or in-house
 molecular methods. These methods vary in time, labour, cost, efficacy and
 adequacy, with some requiring a stepwise process incurring further cost or
 delay. In 1993 Telenti et al. reported an REA ***identification***
 method for ***mycobacteria*** based on a 441bp ***hsp65***
 fragment. Although an important break-through in ***mycobacteria***
 identification, the technique is not without technical and
 interpretative difficulties. DNA sequencing of the Telenti fragment has
 demonstrated great promise for ***identifying*** ***mycobacteria***
 , but previous investigations have been of limited scope. We amplified,
 using the Telenti ***primers***, 78 ***mycobacteria*** putative
 and valid type strains, optimized and sequenced the 401nt region between
 the ***primers*** and loaded these sequences into a local BLAST search
 program to act as a reference library. This library was challenged with
 328 isolates encompassing 28 ***Mycobacterium*** species
 identified by biochemical tests and/or commercial probes.
 hsp65 analysis corroborated the ***identification*** of
 274/328 (83.5%) of the isolates. All isolates of *M. branderi*, *M.*
flavescens, *M. gordonae*, *M. lentiflavum*, *M. marinum*, *M. mucogenicum*, *M.*
obuense, *M. szulgai*, *M. thermoresistibile*, *M. tuberculosis*, or *M. xenopi*,
 were concordant. 71/72 MAC isolates ***identified*** as *M. avium*(54)
 or *M. intracellulare*(17) and 49 *M. gordonae* isolates were assigned to

three groups, type I(15), type 2(22) or type 3(12) as per Brunello et al. Of the 54 discordant isolates 21 purported *M. chelonae* were
 identified by ***hsp65*** as *M. abscessus*(17) or *M. mucogenicum*(4), 12 purported *M. fortuitum* isolates were ***identified*** as *M. chelonae*(1), *M. peregrinum*(10) or *M. mucogenicum*(1) and 21 isolates were associated with the *M. terrae* complex (6), other valid or putative species(8) or were un-assigned(7). We conclude that ***hsp65*** gene sequence is a reliable means for the routine ***identification*** of ***mycobacteria*** ; it is rapid (2 days), does not require mature cultures, is cost effective (approximately dollar sign30USD) and is capable of precise and broad-spectrum ***identifications*** .

TI Rapid ***identification*** of ***Mycobacterium*** species by ***hsp65*** partial gene sequences.

AB Currently, ***Mycobacterium*** species are ***identified*** using biochemical tests, mycolic acid analysis and commercial or in-house molecular methods. These methods vary in time, labour, cost, efficacy. . adequacy, with some requiring a stepwise process incurring further cost or delay. In 1993 Telenti et al. reported an REA ***identification*** method for ***mycobacteria*** based on a 41bp ***hsp65*** fragment. Although an important break- through in ***mycobacteria*** ***identification*** , the technique is not without technical and interpretative difficulties. DNA sequencing of the Telenti fragment has demonstrated great promise for ***identifying*** ***mycobacteria*** , but previous investigations have been of limited scope. We amplified, using the Telenti ***primers*** , 78 ***mycobacteria*** putative and valid type strains, optimized and sequenced the 401nt region between the ***primers*** and loaded these sequences into a local BLAST search program to act as a reference library. This library was challenged with 328 isolates encompassing 28 ***Mycobacterium*** species
 identified by biochemical tests and/or commercial probes. ***hsp65*** analysis corroborated the ***identification*** of 274/328 (83.5%) of the isolates. All isolates of *M. branderi*, *M. flavescens*, *M. gordonae*, *M. lentiflavum*, *M. marinum*, *M. mucogenicum*, *M. obuense*, *M. szulgai*, *M. thermoresistibile*, *M. tuberculosis*, or *M. xenopi*, were concordant. 71/72 MAC isolates ***identified*** as *M. avium*(54) or *M. intracellulare*(17) and 49 *M. gordonae* isolates were assigned to three groups, type I(15), type 2(22) or type 3(12) as per Brunello et al. Of the 54 discordant isolates 21 purported *M. chelonae* were
 identified by ***hsp65*** as *M. abscessus*(17) or *M. mucogenicum*(4), 12 purported *M. fortuitum* isolates were ***identified*** as *M. chelonae*(1), *M. peregrinum*(10) or *M. mucogenicum*(1) and 21 isolates were associated with the *M. terrae* complex (6), other valid or putative species(8) or were un-assigned(7). We conclude that ***hsp65*** gene sequence is a reliable means for the routine ***identification*** of ***mycobacteria*** ; it is rapid (2 days), does not require mature cultures, is cost effective (approximately dollar sign30USD) and is capable of precise and broad-spectrum ***identifications*** .

IT Major Concepts
 Methods and Techniques; Molecular Genetics (Biochemistry and Molecular Biophysics)

II Chemicals & Biochemicals
 Telenti ***primers***

ORGN Classifier
 Mycobacteriaceae 08881
 Super Taxa
 Mycobacteria ; Actinomycetes and Related Organisms;
 Eubacteria; Bacteria; Microorganisms

Organism Name

Mycobacterium (genus): ***identification***
 Mycobacterium avium (species)
 Mycobacterium branderi (species)
 Mycobacterium chelonae (species)
 Mycobacterium flavescens (species)
 Mycobacterium gordonae (species)
 Mycobacterium intracellular (species)
 Mycobacterium lentiflavum (species)
 Mycobacterium marinum (species)
 Mycobacterium mucogenicum (species)
 Mycobacterium obuense (species)
 Mycobacterium peregrinum (species)
 Mycobacterium sp. (species)
 Mycobacterium szulgai (species)
 Mycobacterium terrae (species)
 Mycobacterium thermoresistibile (species)
 Mycobacterium tuberculosis (species)
 Mycobacterium xenopi (species)

Taxa Notes

Bacteria, Eubacteria, Microorganisms

GEN ***hsp65*** gene

L9 ANSWER 11 OF 71 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on
 STN
 AN 2002:188724 BIOSIS <<LOGINID::20090617>>
 DN PREV200200188724
 TI Comparison of biotyping and PCR restriction analysis (PRA) for species
 identification (Sps-ID) of non-tuberculous ***mycobacteria***
 (NTM) in a reference laboratory in Brazil.
 AU Ferrazoli, L. [Reprint author]; Silva, E. C. [Reprint author]; Martins, M.
 C. [Reprint author]; Ueki, S. M. [Reprint author]; Telles, M. A. S.
 [Reprint author]; Smole, S. C.; Leao, S. C.; Arbeit, R. D.
 CS Institut Adolfo Lutz, Sao Paulo, Brazil
 SO Abstracts of the General Meeting of the American Society for Microbiology,
 (2001) Vol. 101, pp. 206. print.
 Meeting Info.: 101st General Meeting of the American Society for
 Microbiology. Orlando, FL, USA. May 20-24, 2001. American Society for
 Microbiology.
 ISSN: 1060-2011.
 DT Conference; (Meeting)
 Conference; Abstract; (Meeting Abstract)
 LA English
 ED Entered STN: 13 Mar 2002
 Last Updated on STN: 13 Mar 2002
 AB Background: Conventional biotyping for Sps-ID of NTM requires up to 4
 weeks and may delay appropriate therapy for NTM infections. This study
 compared Sps-ID by biotyping with PRA of ***hsp65***, the gene
 encoding the 65 kDa heat shock protein, as per Telenti et al. 1993.
 Methods: From Jan 1 to Sept 30, 2000, a total of 298 isolates of NTM were
 processed at Instituto Adolfo Lutz, Sao Paulo, Brazil; 158 were analyzed
 by both methods. For PRA, a 439 bp fragment of ***hsp65*** was
 amplified using ***primers*** TB11 and TB12, digested with HaeIII and
 with BstII, the digests resolved by electrophoresis in 4% agarose, and the
 patterns compared with the available database (<http://www.hospvd.ch:8005>).
 Results: Both methods agreed for 104 (64%) isolates, of which 60 were M.
 avium complex (MAC); 32, M. kansasii; 6, M. fortuitum; 4, M. gordonae; and

2, *M. marinum*. Biotyping was inconclusive for 13 (8%) isolates, of which PRA indicated 3 were MAC and 3 were *M. kansasii*. For 15 (9%) isolates, PRA yielded patterns not in the current databases; of these, biotyping indicated that 7 isolates representing two PRA patterns were *M. goodii*. For 26 (16%) isolates, the two methods gave different Sps-ID. The non-concordant isolates are being resolved by sequencing the entire amplicon from ***hsp65***. Conclusions: PRA provides rapid and reliable Sps-ID for the majority of NTM isolates encountered in a clinical reference laboratory. This should continue to improve as the database of known profiles expands. Further studies, including nucleotide sequencing of the PCR product are in progress to resolve those instances in which PRA and conventional biotyping disagree.

TI Comparison of biotyping and PCR restriction analysis (PRA) for species ***identification*** (Sps-ID) of non-tuberculous ***mycobacteria*** (NTM) in a reference laboratory in Brazil.

AB. . . to 4 weeks and may delay appropriate therapy for NTM infections. This study compared Sps-ID by biotyping with PRA of ***hsp65***, the gene encoding the 65 kDa heat shock protein, as per Telenti et al. 1993. Methods: From Jan 1 to. . . at Instituto Adolfo Lutz, Sao Paulo, Brazil; 158 were analyzed by both methods. For PRA, a 439 bp fragment of ***hsp65*** was amplified using ***primers*** TB11 and TB12, digested with HaeIII and with BstII, the digests resolved by electrophoresis in 4% agarose, and the patterns. . . (16%) isolates, the two methods gave different Sps-ID. The non-concordant isolates are being resolved by sequencing the entire amplicon from ***hsp65***. Conclusions: PRA provides rapid and reliable Sps-ID for the majority of NTM isolates encountered in a clinical reference laboratory. This. . .

IT . . . method, applications, molecular method; polymerase chain reaction restriction analysis technique: analytical method, applications, molecular method

IT Miscellaneous Descriptors
bacterial species ***identification*** : methodologies; clinical reference laboratories; databases; medical ***diagnostics*** ; medical microbiology; therapeutics; Meeting Abstract

ORGN Classifier
Mycobacteriaceae 08881

Super Taxa
Mycobacteria ; Actinomycetes and Related Organisms;
Eubacteria; Bacteria; Microorganisms

Organism Name
Mycobacterium spp.: ***identification*** methods,
non-tuberculous, pathogen

Taxa Notes
Bacteria, Eubacteria, Microorganisms

L9 ANSWER 12 OF 71 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN

AN 2001:409363 BIOSIS <LOGINID:20090617>

DN PREV200100409363

TI The DNA probe and PCR assay as useful tools to control an acid fast bacteria-dependent biotechnological process.

AU Brzostek, Anna M. [Reprint author]; Pawlowicz, Marek; Dziadek, Jaroslaw [Reprint author]

CS Department of Genetics of Microorganisms, Centre for Microbiology and Virology, Polish Academy of Sciences, 106, Lodowa St., 93-232, Lodz, Poland

SO Acta Microbiologica Polonica, (2001) Vol. 50, No. 1, pp. 37-44. print.
ISSN: 0137-1320.

DT Article

LA English

ED Entered STN: 29 Aug 2001
Last Updated on STN: 22 Feb 2002

AB Specific DNA probe has been developed for fast-growing,
mycobacterial mutants able to selectively biotransform side chain
of plant sterols. The PCR assay, using ***primers*** complementary to
the sequence of the probe, was shown to distinguish biotechnological
mutants from other fast-growing ***mycobacteria***. Moreover, the
species ***identification*** of biotechnological strains was done
using PCR-restriction analysis based on amplification and digestion of the
inner part of ***hsp65*** gene (PRA-assay) as well as 16S rRNA
sequencing.

AB Specific DNA probe has been developed for fast-growing,
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species ***identification*** of biotechnological strains was done
using PCR-restriction analysis based on amplification and digestion of the
inner part of ***hsp65*** gene (PRA-assay) as well as 16S rRNA
sequencing.

ORGN Classifier
Bacteria 05000
Super Taxa
Microorganisms
Organism Name
bacteria
Taxa Notes
Bacteria, Eubacteria, Microorganisms

ORGN Classifier
Mycobacteriaceae 08881
Super Taxa
Mycobacteria ; Actinomycetes and Related Organisms;
Eubacteria; Bacteria; Microorganisms
Organism Name
mycobacteria
Taxa Notes
Bacteria, Eubacteria, Microorganisms

GEN ***Mycobacterium*** ***hsp65*** gene (***Mycobacteriaceae***)

L9 ANSWER 13 OF 71 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on
STN

AN 1999:133687 BIOSIS <<LOGINID::20090617>>

DN PREV199900133687

TI Use of restriction enzyme analysis of amplified DNA coding for the
hsp65 gene and polymerase chain reaction with universal
primer for rapid differentiation of ***Mycobacterium***
species in the clinical laboratory.

AU Bahrmand, Ahmad R. [Reprint author]; Bakayeva, Tamara G.; Bakayev, Valery
V.

CS Mycobacteriol. Dep., Pasteur Inst. Iran, Pasteur Ave., Tehran 13164, Iran

SO Scandinavian Journal of Infectious Diseases, (1998) Vol. 30, No. 5, pp.
477-480. print.
CODEN: SJIDB7. ISSN: 0036-5548.

DT Article
 LA English
 ED Entered STN: 31 Mar 1999
 Last Updated on STN: 31 Mar 1999

AB Two rapid procedures, restriction enzyme analysis of the amplified segment of the gene encoding for the 65000 mol. wt heat shock protein and a polymerase chain reaction with single universal ***primer*** (UP-PCR), were used for the ***identification*** of ***Mycobacterium*** tuberculosis complex (n = 47) and proving the species identity of non-tuberculous ***mycobacteria*** (NTM, n = 36) cultured from clinical samples by comparing the resulting DNA banding pattern with patterns derived from ***mycobacterial*** type strains (n = 24). UP-PCR assay provided a rather wide limit of tolerance for variations in procedure. Although ***mycobacterial*** strains were found to generate species-specific banding patterns in both assays, M. tuberculosis and M. bovis strains and isolates produced nearly the same DNA patterns, which were very distinctive from that of all NTM tested. Investigation of the majority of M. fortuitum (n = 14) and M. kansasii (n = 7), ***mycobacteria*** most frequently causing ***mycobacterioses*** in the region, as well as other NTM isolates, showed reproducible patterns characteristic of corresponding type strains. Both methods combine the advantages of ordinary PCR and PCR 'fingerprinting', namely, the species-specific DNA pattern and ***primers*** applicable to different species. They may be applied as rapid tests for proving the identity of ***Mycobacterium*** species in a clinical laboratory.

TI Use of restriction enzyme analysis of amplified DNA coding for the ***hsp65*** gene and polymerase chain reaction with universal ***primer*** for rapid differentiation of ***Mycobacterium*** species in the clinical laboratory.

AB. . . of the gene encoding for the 65000 mol. wt heat shock protein and a polymerase chain reaction with single universal ***primer*** (UP-PCR), were used for the ***identification*** of ***Mycobacterium*** tuberculosis complex (n = 47) and proving the species identity of non-tuberculous ***mycobacteria*** (NTM, n = 36) cultured from clinical samples by comparing the resulting DNA banding pattern with patterns derived from ***mycobacterial*** type strains (n = 24). UP-PCR assay provided a rather wide limit of tolerance for variations in procedure. Although ***mycobacterial*** strains were found to generate species-specific banding patterns in both assays, M. tuberculosis and M. bovis strains and isolates produced. . . of all NTM tested. Investigation of the majority of M. fortuitum (n = 14) and M. kansasii (n = 7), ***mycobacteria*** most frequently causing ***mycobacterioses*** in the region, as well as other NTM isolates, showed reproducible patterns characteristic of corresponding type strains. Both methods combine the advantages of ordinary PCR and PCR 'fingerprinting', namely, the species-specific DNA pattern and ***primers*** applicable to different species. They may be applied as rapid tests for proving the identity of ***Mycobacterium*** species in a clinical laboratory.

IT . . . Concepts
 Clinical Chemistry (Allied Medical Sciences); Infection; Molecular Genetics (Biochemistry and Molecular Biophysics)

IT Chemicals & Biochemicals
 DNA: analysis, bacterial; ***Mycobacterium*** ***hsp65*** gene

IT Methods & Equipment
 polymerase chain reaction: DNA amplification, bacteria
 identification method, molecular genetic method,

diagnostic method, sequencing techniques, analytical method;
 restriction enzyme analysis: analytical method, bacteria
 identification method, ***diagnostic*** method, molecular
 genetic method
 ORGN . . .
 Taxa
 Primates; Mammalia; Vertebrata; Chordata; Animalia
 Organism Name
 human: patient
 Taxa Notes
 Animals, Chordates, Humans, Mammals, Primates, Vertebrates
 ORGN Classifier
 Mycobacteriaceae 08881
 Super Taxa
 Mycobacteria ; Actinomycetes and Related Organisms;
 Eubacteria; Bacteria; Microorganisms
 Organism Name
 Mycobacterium bovis: pathogen
 Mycobacterium fortuitum: pathogen
 Mycobacterium spp.: pathogen
 Taxa Notes
 Bacteria, Eubacteria, Microorganisms

L9 ANSWER 14 OF 71 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on
 STN
 AN 1992:391344 BIOSIS <<LOGINID::20090617>>
 DN PREV199294063519; BA94:63519
 TI DIFFERENTIATION OF SLOWLY GROWING ***MYCOBACTERIUM*** -SPP INCLUDING
 MYCOBACTERIUM -TUBERCULOSIS BY GENE AMPLIFICATION AND RESTRICTION
 FRAGMENT LENGTH POLYMORPHISM ANALYSIS.
 AU PLIKAYTIS B B [Reprint author]; PLIKAYTIS B D; YAKRUS M A; BUTLER W R;
 WOODLEY C L; SILCOX V A; SHINNICK T M
 CS DIVISION BACTERIAL MYCOTIC DISEASES, NATIONAL CENTER INFECTIOUS DISEASES,
 CENTERS DISEASE CONTROL, ATLANTA, GA 30333, USA
 SO Journal of Clinical Microbiology, (1992) Vol. 30, No. 7, pp. 1815-1822.
 CODEN: JCMIDW. ISSN: 0095-1137.
 DT Article
 FS BA
 LA ENGLISH
 ED Entered STN: 24 Aug 1992
 Last Updated on STN: 24 Aug 1992
 AB A two-step assay combining a gene amplification step and a restriction
 fragment length polymorphism analysis was developed to differentiate the
 Mycobacterium species that account for > 90% of potentially
 pathogenic isolates and >86% of all isolates in clinical laboratories in
 the United States. These species are *M. tuberculosis*, *M. bovis*, *M. avium*,
M. intracellulare, *M. kansasii*, and *M. goodii*. With lysates of pure
 cultures as the template, two oligonucleotide ***primers*** that
 amplified an approx. 1,380-bp portion of the ***hsp65*** gene from all
 139 strains of 19 ***Mycobacterium*** species tested, but not from the
 19 non- ***Mycobacterium*** species tested, were ***identified***.
 Digestion of the amplicons from 126 strains of the six most commonly
 isolated ***Mycobacterium*** species with the restriction enzymes
*Bst*NI and *Xho*I in separate reactions generated restriction fragment
 patterns that were distinctive for each of these species, except for those
 of *M. tuberculosis* and *M. bovis*, which were not distinguishable. By
 including size standards in each sample, the restriction fragment profiles

could be normalized to a fixed distance and the similarities of patterns could be calculated by using a computer-aided comparison program. The availability of this data base should enable the ***identification*** of an unknown ***Mycobacterium*** strain to the species level by a comparison of the restriction fragment pattern of the unknown with the data base of known patterns.

TI DIFFERENTIATION OF SLOWLY GROWING ***MYCOBACTERIUM*** -SPP INCLUDING ***MYCOBACTERIUM*** -TUBERCULOSIS BY GENE AMPLIFICATION AND RESTRICTION FRAGMENT LENGTH POLYMORPHISM ANALYSIS.

AB. . . A two-step assay combining a gene amplification step and a restriction fragment length polymorphism analysis was developed to differentiate the ***Mycobacterium*** species that account for > 90% of potentially pathogenic isolates and >86% of all isolates in clinical laboratories in the . . . bovis, M. avium, M. intracellulare, M. kansasii, and M. gordonae. With lysates of pure cultures as the template, two oligonucleotide ***primers*** that amplified an .apprx.1,380-bp portion of the ***hsp65*** gene from all 139 strains of 19 ***Mycobacterium*** species tested, but not from the 19 non-***Mycobacterium*** species tested, were ***identified***. Digestion of the amplicons from 126 strains of the six most commonly isolated ***Mycobacterium*** species with the restriction enzymes BstNI and XhoI in separate reactions generated restriction fragment patterns that were distinctive for each. . . of patterns could be calculated by using a computer-aided comparison program. The availability of this data base should enable the ***identification*** of an unknown ***Mycobacterium*** strain to the species level by a comparison of the restriction fragment pattern of the unknown with the data base. . .

IT Miscellaneous Descriptors
 MYCOBACTERIUM -BOVIS ***MYCOBACTERIUM*** -AVIUM
 MYCOBACTERIUM -INTRACELLULARE ***MYCOBACTERIUM*** -KANSASII
 MYCOBACTERIUM -GORDONAE MOLECULAR ***DIAGNOSTIC*** METHOD
 COMPUTER AIDED COMPARISON

ORGN Classifier
 Mycobacteriaceae 08881
 Super Taxa
 Mycobacteria ; Actinomycetes and Related Organisms;
 Eubacteria; Bacteria; Microorganisms
 Taxa Notes
 Bacteria, Eubacteria, Microorganisms

L9 ANSWER 15 OF 71 CABA COPYRIGHT 2009 CABI on STN
 AN 2008:76969 CABA <<LOGINID:20090617>>
 DN 20083066496

TI Molecular characterization of a novel fastidious ***mycobacterium*** causing lepromatous lesions of the skin, subcutis, cornea, and conjunctiva of cats living in Victoria, Australia

AU Fyfe, J. A.; McCowan, C.; O'Brien, C. R.; Globan, M.; Birch, C.; Revill, P.; Barrs, V. R. D.; Wayne, J.; Hughes, M. S.; Holloway, S.; Malik, R.

CS Victorian Infectious Diseases Reference Laboratory, 10 Wreckyn St., North Melbourne, Victoria 3051, Australia. janet.fyfe@mh.org.au

SO Journal of Clinical Microbiology, (2008) Vol. 46, No. 2, pp. 618-626. 27 ref.
 Publisher: American Society for Microbiology (ASM). Washington
 ISSN: 0095-1137
 URL: <http://jcm.asm.org/>

CY United States
 DT Journal

LA English
ED Entered STN: 4 Apr 2008
Last Updated on STN: 4 Apr 2008

AB Between 1999 and 2006, 15 cats were ***diagnosed*** with disease attributable to a novel ***mycobacterial*** species. The infections consisted of granulomatous lesions in the skin, subcutis, and ocular or periocular tissues with an indolent but progressive clinical course. Lesions typically were found in facial regions or on the distal limbs. Cats of all ages and both sexes were affected. Infections often were challenging to treat, although they could be cured using surgery in concert with combination antimicrobial therapy. Microscopically, lesions were granulomatous to pyogranulomatous and contained numerous acid-fast bacilli. Scanty cultures of the causal microorganisms occasionally could be obtained in ***mycobacterial*** broth, but subculture to solid media failed. When cultures were not available, DNA was extracted from fresh tissue, lyophilized material, and formalin-fixed, paraffin-embedded tissues from lesions. PCR amplification of the 5[prime] end of the 16S rRNA gene and regions within four additional loci (ITS1, ***hsp65***, rpoB, and sodA) was performed with various efficiencies using ***mycobacterial*** primers. Nucleotide sequences were unique for each locus tested. Nucleotide sequences obtained from individual cases were identical for each locus for which the amplification was successful. Phylogenetic analysis performed using concatenated partial 16S rRNA and ***hsp65*** gene sequences indicated that this novel ***mycobacterial*** species from Victoria is a member of the ***Mycobacterium*** simiae-related group, taxonomically related to the ***mycobacterium*** causing leproid granulomas in dogs throughout the world. Based on the clustering of cases, we refer to this novel species as ***Mycobacterium*** sp. strain Tarwin.

TI Molecular characterization of a novel fastidious ***mycobacterium*** causing lepromatous lesions of the skin, subcutis, cornea, and conjunctiva of cats living in Victoria, Australia.

AB Between 1999 and 2006, 15 cats were ***diagnosed*** with disease attributable to a novel ***mycobacterial*** species. The infections consisted of granulomatous lesions in the skin, subcutis, and ocular or periocular tissues with an indolent but. . . were granulomatous to pyogranulomatous and contained numerous acid-fast bacilli. Scanty cultures of the causal microorganisms occasionally could be obtained in ***mycobacterial*** broth, but subculture to solid media failed. When cultures were not available, DNA was extracted from fresh tissue, lyophilized material, . . . from lesions. PCR amplification of the 5[prime] end of the 16S rRNA gene and regions within four additional loci (ITS1, ***hsp65***, rpoB, and sodA) was performed with various efficiencies using ***mycobacterial*** primers. Nucleotide sequences were unique for each locus tested. Nucleotide sequences obtained from individual cases were identical for each locus for which the amplification was successful. Phylogenetic analysis performed using concatenated partial 16S rRNA and ***hsp65*** gene sequences indicated that this novel ***mycobacterial*** species from Victoria is a member of the ***Mycobacterium*** simiae-related group, taxonomically related to the ***mycobacterium*** causing leproid granulomas in dogs throughout the world. Based on the clustering of cases, we refer to this novel species as ***Mycobacterium*** sp. strain Tarwin.

BT. . . Australasia; Oceania; Developed Countries; Commonwealth of Nations; OECD Countries; Felis; Felidae; Fissipeda; carnivores; mammals; vertebrates; Chordata; animals; small mammals; eukaryotes; ***Mycobacteriaceae*** ; Firmicutes; bacteria; prokaryotes;

Mycobacterium ; Australia
ST bacterial infections; bacterioses; clinical picture; ***Mycobacterium***
simiae; rRNA
ORGN cats; ***Mycobacterium***

L9 ANSWER 16 OF 71 CAPLUS COPYRIGHT 2009 ACS on STN
AN 2009:601805 CAPLUS <<LOGINID::20090617>>
TI Cloning and sequence analysis of ***Mycobacterium*** paratuberculosis
hsp65 gene
AU Xu, Feng-yu; Hu, Yu-qing; Zeng, Fan-li; Jiang, Xiu-yun; He, Zhao-yang
CS College of Animal Science and Technology, Jilin Agricultural University,
Changchun, 130118, Peop. Rep. China
SO Jilin Nongye Daxue Xuebao (2009), 31(2), 204-207
CODEN: JNDXE8; ISSN: 1000-5684
PB Jilin Nongye Daxue Xuebao Bianjibu
DT Journal
LA Chinese
AB The genomic DNA was extd. from ***Mycobacterium***
paratuberculosis(MP) strain C - 2. The secreted protein ***hsp65***
gene was amplified with a pair of specific ***primers*** using
polymerase chain reaction (PCR). PCR product was an approximate 1 626 bp
DNA segment. The clone vector pGEM-T- ***hsp65*** was constructed
successfully by the PCR product that was cloned into pGEM-T vector using T
- A clone technique, and the recombinant clone was ***identified*** by
using complementation test, plasmid size test, restriction enzyme assay,
plasmid PCR ***identification*** and recombinant plasmid sequence
anal. The anal. indicated that the ***hsp65*** gene was very
conservative in MP. These results could serve as a basis for further
study on the usefulness of ***hsp65*** gene and immunogenicity
characteristic of ***hsp65*** gene expression product.
TI Cloning and sequence analysis of ***Mycobacterium*** paratuberculosis
hsp65 gene
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anal. The anal. indicated that the ***hsp65*** gene was very
conservative in MP. These results could serve as a basis for further
study on the usefulness of ***hsp65*** gene and immunogenicity
characteristic of ***hsp65*** gene expression product.

L9 ANSWER 17 OF 71 CAPLUS COPYRIGHT 2009 ACS on STN
AN 2008:1297669 CAPLUS <<LOGINID::20090617>>
DN 149:508418
TI Immunological capture and PCR detection of ***Mycobacteria*** from
environmental samples
IN Kluge, Christoph; Gutierrez Perez, Maria-Cristina; Marchal, Gilles
PA Institut Pasteur, Fr.; Centre d'Analyses Environnementales (CAE)
SO Can. Pat. Appl., 68pp.
CODEN: CPXXEB
DT Patent
LA English

FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	CA 2629465	A1	20081019	CA 2008-2629465	20080418
	CA 2585670	A1	20081019	CA 2007-2585670	20070419
	CA 2618289	A1	20081019	CA 2008-2618289	20080121
	WO 2008129419	A2	20081030	WO 2008-IB1255	20080421
	WO 2008129419	A3	20090430		

W: AE, AG, AL, AM, AO, AT, AU, AZ, BA, BB, BG, BH, BR, BW, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DO, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, GT, HN, HR, HU, ID, IL, IN, IS, JP, KE, KG, KM, KN, KP, KR, KZ, LA, LC, LK, LR, LS, LT, LU, LY, MA, MD, ME, MG, MK, MN, MW, MX, MY, MZ, NA, NG, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RS, RU, SC, SD, SE, SG, SK, SL, SM, SV, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, ZA, ZM, ZW

RW: AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HR, HU, IE, IS, IT, LT, LU, LV, MC, MT, NL, NO, PL, PT, RO, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG, BW, GH, GM, KE, LS, MW, MZ, NA, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AP, EA, EP, OA

PRAI CA 2007-2585670 A 20070419
CA 2008-2618289 A 20080121

AB Methods of detecting and isolating ***Mycobacteria*** from the environment are described. The method can be applied to non-tuberculosis ***Mycobacteria*** that may pose a health risk to the elderly and immunocompromised. The ***Mycobacteria*** are selectively captured using antibodies immobilized on magnetic particles. They can then be quantified by PCR of a marker gene such as sodA. Use of polyclonal antibodies is demonstrated. The method can detect 100 cfu of ***Mycobacterium*** in six hours.

TI Immunological capture and PCR detection of ***Mycobacteria*** from environmental samples

AB Methods of detecting and isolating ***Mycobacteria*** from the environment are described. The method can be applied to non-tuberculosis ***Mycobacteria*** that may pose a health risk to the elderly and immunocompromised. The ***Mycobacteria*** are selectively captured using antibodies immobilized on magnetic particles. They can then be quantified by PCR of a marker gene such as sodA. Use of polyclonal antibodies is demonstrated. The method can detect 100 cfu of ***Mycobacterium*** in six hours.

ST ***Mycobacterium*** detection immobilized antibody PCR

IT Cell wall
(***Mycobacterium*** , antibodies to; immunol. capture and PCR detection of ***Mycobacteria*** from environmental samples)

IT Oryctolagus cuniculus
Rabbit
(anti- ***Mycobacterium*** antibodies from; immunol. capture and PCR detection of ***Mycobacteria*** from environmental samples)

IT Magnetic particles
(anti- ***Mycobacterium*** antibodies immobilized on; immunol. capture and PCR detection of ***Mycobacteria*** from environmental samples)

IT Biofilms (microbial)
Drinking waters
Environmental analysis
Milk
Sputum

Waters
 (detection of ***Mycobacterium*** in; immunol. capture and PCR
 detection of ***Mycobacteria*** from environmental samples)

IT Food analysis
 (detection of non-tuberculosis ***Mycobacterium*** in; immunol.
 capture and PCR detection of ***Mycobacteria*** from environmental
 samples)

IT ***Mycobacterium*** BCG
 Mycobacterium abscessus
 Mycobacterium avium
 Mycobacterium gordonae
 Mycobacterium kansasii
 Mycobacterium xenopi
 (detection of; immunol. capture and PCR detection of
 Mycobacteria from environmental samples)

IT Enzyme-linked immunosorbent assay
 Immunoassay
 (for ***Mycobacterium*** ; immunol. capture and PCR detection of
 Mycobacteria from environmental samples)

IT ***Primers*** (nucleic acid)
 RL: ARG (Analytical reagent use); DGN (Diagnostic use); PRP (Properties);
 ANST (Analytical study); BIOL (Biological study); USES (Uses)
 (for detection of ***Mycobacterium*** ; immunol. capture and PCR
 detection of ***Mycobacteria*** from environmental samples)

IT Gene, microbial
 RL: ANT (Analyte); ANST (Analytical study)
 (gyrA, as marker in detection of ***Mycobacterium*** by PCR;
 immunol. capture and PCR detection of ***Mycobacteria*** from
 environmental samples)

IT Gene, microbial
 RL: ANT (Analyte); ANST (Analytical study)
 (***hsp65*** , as marker in detection of ***Mycobacterium*** by
 PCR; immunol. capture and PCR detection of ***Mycobacteria*** from
 environmental samples)

IT Antibodies and Immunoglobulins
 RL: ARG (Analytical reagent use); DGN (Diagnostic use); ANST (Analytical
 study); BIOL (Biological study); USES (Uses)
 (immobilized, to ***Mycobacterium*** ; immunol. capture and PCR
 detection of ***Mycobacteria*** from environmental samples)

IT ***Mycobacterium***
 (immunol. capture and PCR detection of ***Mycobacteria*** from
 environmental samples)

IT Gene, microbial
 RL: ANT (Analyte); ANST (Analytical study)
 (inhA, as marker in detection of ***Mycobacterium*** by PCR;
 immunol. capture and PCR detection of ***Mycobacteria*** from
 environmental samples)

IT ***Diagnosis***
 (mol., of non-tuberculosis ***Mycobacterial*** infection; immunol.
 capture and PCR detection of ***Mycobacteria*** from environmental
 samples)

IT Bacterial infection
 (non-tuberculosis ***Mycobacterium*** , ***diagnosis*** of;
 immunol. capture and PCR detection of ***Mycobacteria*** from
 environmental samples)

IT Polymerase chain reaction
 (quant., for detection of ***Mycobacterium*** ; immunol. capture and

PCR detection of ***Mycobacteria*** from environmental samples)

IT Gene, microbial
 RL: ANT (Analyte); ANST (Analytical study)
 (sodA, as marker in detection of ***Mycobacterium*** by PCR;
 immunol. capture and PCR detection of ***Mycobacteria*** from
 environmental samples)

IT 1072990-26-1 1072990-27-2 1072990-28-3 1072990-29-4 1072990-30-7
 1072990-31-8 1072990-32-9 1072990-33-0 1072990-34-1 1072990-35-2
 1072990-36-3 1072990-37-4
 RL: ARG (Analytical reagent use); DGN (Diagnostic use); PRP (Properties);
 ANST (Analytical study); BIOL (Biological study); USES (Uses)
 (***primer*** for detection of ***Mycobacterium*** ; immunol.
 capture and PCR detection of ***Mycobacteria*** from environmental
 samples)

L9 ANSWER 18 OF 71 CAPLUS COPYRIGHT 2009 ACS on STN

AN 2008:1230479 CAPLUS <LOGINID::20090617>

TI Detection and characterization of nocardia from patients ***diagnosed***
 as tuberculosis in Egypt

AU Helal, Zeinab H.; Khan, Mazhar I.; El-Din Ashour, Mohamed Seif; Eissa,
 Somaia A.

CS Department of Microbiology and Immunology, Faculty of Pharmacy, Al-Azhar
 University, Cairo, Egypt

SO International Journal of Biomedical Science (Monterey Park, CA, United
 States) (2008), 4(3), 179-184
 CODEN: IJBSDB; ISSN: 1550-9702

PB Master Publishing Group

DT Journal

LA English

AB Pulmonary tuberculosis and pulmonary nocardiosis are similar in most clin.
 symptoms and radiol. manifestation. In the developing countries like
 Egypt where tuberculosis is very common, anti-tuberculosis drugs are
 started on basis of radiol. and clin. symptoms. This study included 600
 sputum specimens collected from 200 patients ***diagnosed*** as
 pulmonary tuberculosis from three chest hospitals in Egypt. IS6110
 specific ***primer*** were selected for PCR to ***identify*** the
 Mycobacterium tuberculosis and ***hsp65*** gene specific
 primers were used for PCR and sequencing for the
 identification of ***Mycobacterium*** and Nocardial species.
 The region of the gene coding for 16S rRNA in Nocardia species were
 selected as genus specific ***primer*** sequences for a PCR and Real
 Time PCR assays. Our result confirmed that four whole DNA samples, extd.
 from sputum specimen from the pulmonary tuberculosis patients on
 anti-tuberculosis treatment, were Nocardia species. Three of them matched
 (99% homol.) with Nocardia farcinica (formerly Nocardia asteroid type V)
 and one match (83% homol.) with Nocardia pneumonia. Mol. methods such as
 PCR and real-time PCR for ***identification*** of Nocardia are rapid
 and accurate methods. No cross-reactions were obsd. using Real Time PCR
 specific for Nocardia with other closely related genera.

RE.CNT 25 THERE ARE 25 CITED REFERENCES AVAILABLE FOR THIS RECORD
 ALL CITATIONS AVAILABLE IN THE RE FORMAT

TI Detection and characterization of nocardia from patients ***diagnosed***
 as tuberculosis in Egypt

AB . . . drugs are started on basis of radiol. and clin. symptoms. This
 study included 600 sputum specimens collected from 200 patients
 diagnosed as pulmonary tuberculosis from three chest hospitals in
 Egypt. IS6110 specific ***primer*** were selected for PCR to

identify the ***Mycobacterium*** tuberculosis and
 hsp65 gene specific ***primers*** were used for PCR and
 sequencing for the ***identification*** of ***Mycobacterium*** and
 Nocardial species. The region of the gene coding for 16S rRNA in Nocardia
 species were selected as genus specific ***primer*** sequences for a
 PCR and Real Time PCR assays. Our result confirmed that four whole DNA
 samples, extd. from sputum. . . asteroid type V) and one match (83%
 homol.) with Nocardia pneumonia. Mol. methods such as PCR and real-time
 PCR for ***identification*** of Nocardia are rapid and accurate
 methods. No cross-reactions were obsd. using Real Time PCR specific for
 Nocardia with other. . .

ST Nocardia ***Mycobacterium*** pulmonary tuberculosis
 IT INDEXING IN PROGRESS
 IT INDEXING IN PROGRESS
 IT rRNA
 (16 S; detection and characterization of Nocardia from patients
 diagnosed as tuberculosis in Egypt)

IT Human
 Mycobacterium tuberculosis
 Tuberculosis
 (detection and characterization of Nocardia from patients
 diagnosed as tuberculosis in Egypt)

L9 ANSWER 19 OF 71 CAPLUS COPYRIGHT 2009 ACS ON STN
 AN 2008:962412 CAPLUS <<LOGINID:20090617>>
 DN 150:275953
 TI A single-step sequencing method for the ***identification*** of
 Mycobacterium tuberculosis complex species
 AU Djelouadj, Zoheira; Raoult, Didier; Daffe, Mamadou; Drancourt, Michel
 CS Unite des Rickettsies CNRS UMR6020, IFR 48, Faculte de Medecine,
 Universite de la Mediterranee, Marseille, Fr.
 SO PLoS Neglected Tropical Diseases (2008), 2(6), No pp. given
 CODEN: PNIDAM; ISSN: 1935-2735
 URL: <http://www.plosntds.org/article/info%3Adoi%2F10.1371%2Fjournal.pntd.000253>
 PB Public Library of Science
 DT Journal; (online computer file)
 LA English
 AB The ***Mycobacterium*** tuberculosis complex (MTC) comprises closely
 related species responsible for strictly human and zoonotic tuberculosis.
 Accurate species detn. is useful for the ***identification*** of
 outbreaks and epidemiol. links. ***Mycobacterium*** africanum and
 Mycobacterium canettii are typically restricted to Africa and M.
 bovis is a re-emerging pathogen. ***Identification*** of these
 species is difficult and expensive. The Exact Tandem Repeat D (ETR-D;
 alias ***Mycobacterial*** Interspersed Repetitive Unit 4) was
 sequenced in MTC species type strains and 110 clin. isolates, in parallel
 to ref. polyphasic ***identification*** based on phenotype profiling
 and sequencing of pncA, oxyR, ***hsp65***, gyrB genes and the major
 polymorphism tandem repeat. Inclusion of M. tuberculosis isolates in the
 expanding, antibiotic-resistant Beijing clone was detd. by Rv0927c gene
 sequencing. The ETR-D (780-bp) sequence unambiguously ***identified***
 MTC species type strain except M. pinnipedii and M. microti due to six
 single nucleotide polymorphisms, variable nos. (1-7 copies) of the tandem
 repeat and two deletions/insertions. The ETR-D sequencing agreed with
 phenotypic ***identification*** in 107/110 clin. isolates and with
 ref. polyphasic mol. ***identification*** in all isolates, comprising

98 M. tuberculosis, 5 M. bovis BCG type, 5 M. canettii, and 2 M. africanum. For M. tuberculosis isolates, the ETR-D sequence was not significantly assocd. with the Beijing clone. ETR-D sequencing allowed accurate, single-step ***identification*** of the MTC at the species level. It circumvented the current expensive, time-consuming polyphasic approach. It could be used to depict epidemiol. of zoonotic and human tuberculosis, esp. in African countries where several MTC species are emerging.

RE.CNT 70 THERE ARE 70 CITED REFERENCES AVAILABLE FOR THIS RECORD

ALL CITATIONS AVAILABLE IN THE RE FORMAT

- TI A single-step sequencing method for the ***identification*** of
 Mycobacterium tuberculosis complex species
- AB The ***Mycobacterium*** tuberculosis complex (MTC) comprises closely related species responsible for strictly human and zoonotic tuberculosis. Accurate species detn. is useful for the ***identification*** of outbreaks and epidemiol. links. ***Mycobacterium*** africanum and ***Mycobacterium*** canettii are typically restricted to Africa and M. bovis is a re-emerging pathogen. ***Identification*** of these species is difficult and expensive. The Exact Tandem Repeat D (ETR-D; alias ***Mycobacterial*** Interspersed Repetitive Unit 4) was sequenced in MTC species type strains and 110 clin. isolates, in parallel to ref. polyphasic ***identification*** based on phenotype profiling and sequencing of pncA, oxyR, ***hsp65***, gyrB genes and the major polymorphism tandem repeat. Inclusion of M. tuberculosis isolates in the expanding, antibiotic-resistant Beijing clone was detd. by Rv0927c gene sequencing. The ETR-D (780-bp) sequence unambiguously ***identified*** MTC species type strain except M. pinnipedii and M. microti due to six single nucleotide polymorphisms, variable nos. (1-7 copies) of the tandem repeat and two deletions/insertions. The ETR-D sequencing agreed with phenotypic ***identification*** in 107/110 clin. isolates and with ref. polyphasic mol. ***identification*** in all isolates, comprising 98 M. tuberculosis, 5 M. bovis BCG type, 5 M. canettii, and 2 M. africanum. For M. tuberculosis isolates, the ETR-D sequence was not significantly assocd. with the Beijing clone. ETR-D sequencing allowed accurate, single-step ***identification*** of the MTC at the species level. It circumvented the current expensive, time-consuming polyphasic approach. It could be used to. . .
- ST PCR exact tandem repeat D ***Mycobacterium*** species
 identification; DNA sequence Senx3 Regx3 intergenic spacer ETRD repeat ***Mycobacterium***; sequence DNA gene oxyR ***hsp65***
 Mycobacterium; ***primer*** PCR DNA repeat ETRD
 Mycobacterium species ***identification***
- II ***Primers*** (nucleic acid)
 RL: ARG (Analytical reagent use); BUU (Biological use, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
 (DNA; ETR-D sequencing for single-step ***identification*** of
 Mycobacterium tuberculosis complex at species level, and its comparison with sequencing of housekeeping genes and polymorphism tandem repeat)
- II Cell morphology
 Phenotypes
 (ETR-D sequencing for single-step ***identification*** of
 Mycobacterium tuberculosis complex at species level, and its comparison with sequencing of housekeeping genes and phenotypic characteristics)
- II ***Mycobacterium*** tuberculosis

Polymerase chain reaction
 (ETR-D sequencing for single-step ***identification*** of
 Mycobacterium tuberculosis complex at species level, and its
 comparison with sequencing of housekeeping genes and polymorphism
 tandem repeat)

IT Heat-shock proteins
 RL: BSU (Biological study, unclassified); PRP (Properties); BIOL
 (Biological study)
 (HSP 65; partial DNA and amino acid sequences of novel oxyR,
 hsp65 and mptR genes found in ***Mycobacterium*** canettii
 and M. africanum)

IT Genetic element
 RL: ANT (Analyte); BUU (Biological use, unclassified); DGN (Diagnostic
 use); PRP (Properties); ANST (Analytical study); BIOL (Biological study);
 USES (Uses)
 (IGS (intergenic spacer), ETR-D repeat located in Senx3-Regx3 spacer
 region; partial DNA and amino acid sequences of ***Mycobacterium***
 genes Senx3 and Regx3, including the Senx3-Regx3 intergenic spacer that
 contains the ETR-D repeat)

IT Genetic polymorphism
 (INDEL; ETR-D sequencing for single-step ***identification*** of
 Mycobacterium tuberculosis complex at species level, and its
 comparison with sequencing of housekeeping genes and phenotypic
 characteristics)

IT Transcription factors
 RL: BSU (Biological study, unclassified); PRP (Properties); BIOL
 (Biological study)
 (OxyR; partial DNA and amino acid sequences of novel oxyR,
 hsp65 and mptR genes found in ***Mycobacterium*** canettii
 and M. africanum)

IT Gene, microbial
 RL: BSU (Biological study, unclassified); PRP (Properties); BIOL
 (Biological study)
 (Regx3, Senx3-Regx3 spacer region; partial DNA and amino acid sequences
 of ***Mycobacterium*** genes Senx3 and Regx3, including the
 Senx3-Regx3 intergenic spacer that contains the ETR-D repeat)

IT Gene, microbial
 RL: BSU (Biological study, unclassified); PRP (Properties); BIOL
 (Biological study)
 (Senx3, Senx3-Regx3 spacer region; partial DNA and amino acid sequences
 of ***Mycobacterium*** genes Senx3 and Regx3, including the
 Senx3-Regx3 intergenic spacer that contains the ETR-D repeat)

IT Proteins
 RL: BSU (Biological study, unclassified); PRP (Properties); BIOL
 (Biological study)
 (gene Regx3, sensory transduction protein, sequence homolog; partial
 DNA and amino acid sequences of ***Mycobacterium*** genes Senx3 and
 Regx3, including the Senx3-Regx3 intergenic spacer that contains the
 ETR-D repeat)

IT Proteins
 RL: BSU (Biological study, unclassified); PRP (Properties); BIOL
 (Biological study)
 (gene mptR; partial DNA and amino acid sequences of novel oxyR,
 hsp65 and mptR genes found in ***Mycobacterium*** canettii
 and M. africanum)

IT Gene, microbial
 RL: ANT (Analyte); BUU (Biological use, unclassified); DGN (Diagnostic

use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
 (gyrB; partial DNA sequences and SNPs of five housekeeping genes (pncA, oxyR, ***hsp65***, gyrB and mptR) from eight ***Mycobacterium*** tuberculosis complex strains)

IT Gene, microbial
 RL: ANT (Analyte); BUU (Biological use, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
 (***hsp65*** ; partial DNA sequences and SNPs of five housekeeping genes (pncA, oxyR, ***hsp65***, gyrB and mptR) from eight ***Mycobacterium*** tuberculosis complex strains)

IT ***Diagnosis***
 (mol.; ETR-D sequencing for single-step ***identification*** of ***Mycobacterium*** tuberculosis complex at species level, and its comparison with sequencing of housekeeping genes and phenotypic characteristics)

IT Gene, microbial
 RL: ANT (Analyte); BUU (Biological use, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
 (mptR; partial DNA sequences and SNPs of five housekeeping genes (pncA, oxyR, ***hsp65***, gyrB and mptR) from eight ***Mycobacterium*** tuberculosis complex strains)

IT Gene, microbial
 RL: ANT (Analyte); BUU (Biological use, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
 (oxyR; partial DNA sequences and SNPs of five housekeeping genes (pncA, oxyR, ***hsp65***, gyrB and mptR) from eight ***Mycobacterium*** tuberculosis complex strains)

IT DNA sequences
 Mycobacterium BCG
 Mycobacterium africanum
 Mycobacterium bovis
 Mycobacterium canettii
 Mycobacterium caprae
 Mycobacterium microti
 Mycobacterium pinnipedii

Protein sequences
 (partial DNA and amino acid sequences of ***Mycobacterium*** genes Senx3 and Regx3, including the Senx3-Regx3 intergenic spacer that contains the ETR-D repeat)

IT Single nucleotide polymorphism
 (partial DNA sequences and SNPs of five housekeeping genes (pncA, oxyR, ***hsp65***, gyrB and mptR) from eight ***Mycobacterium*** tuberculosis complex strains)

IT Gene, microbial
 RL: ANT (Analyte); BUU (Biological use, unclassified); DGN (Diagnostic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
 (pncA; partial DNA sequences and SNPs of five housekeeping genes (pncA, oxyR, ***hsp65***, gyrB and mptR) from eight ***Mycobacterium*** tuberculosis complex strains)

IT DNA
 RL: ARG (Analytical reagent use); BUU (Biological use, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
 (***primer*** ; ETR-D sequencing for single-step

identification of ***Mycobacterium*** tuberculosis complex at species level, and its comparison with sequencing of housekeeping genes and polymorphism tandem repeat)

II Repetitive DNA
 RL: ANT (Analyte); BUU (Biological use, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
 (tandem, exact D, ETR-D in Senx3-Regx3 intergenic spacer; ETR-D sequencing for single-step ***identification*** of ***Mycobacterium*** tuberculosis complex at species level, and its comparison with sequencing of housekeeping genes and polymorphism tandem repeat)

II Repetitive DNA
 RL: ANT (Analyte); BUU (Biological use, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
 (tandem; ETR-D sequencing for single-step ***identification*** of ***Mycobacterium*** tuberculosis complex at species level, and its comparison with sequencing of housekeeping genes and polymorphism tandem repeat)

II 1124387-63-8 1124387-64-9
 RL: ARG (Analytical reagent use); BUU (Biological use, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
 (ETR-D-specific ***primer***; ETR-D sequencing for single-step ***identification*** of ***Mycobacterium*** tuberculosis complex at species level, and its comparison with sequencing of housekeeping genes and polymorphism tandem repeat)

II 1123333-08-3 1123333-09-4 1123333-11-8 1123333-12-9 1123333-14-1
 1123333-15-2 1123333-17-4 1123333-18-5 1123333-20-9 1123333-21-0
 1123333-23-2 1123333-24-3 1123333-26-5 1123333-27-6
 RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
 (amino acid sequence; partial DNA and amino acid sequences of ***Mycobacterium*** genes Senx3 and Regx3, including the Senx3-Regx3 intergenic spacer that contains the ETR-D repeat)

II 1088759-76-5 1088759-78-7 1088759-80-1
 RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
 (amino acid sequence; partial DNA and amino acid sequences of novel oxyR, ***hsp65*** and mptR genes found in ***Mycobacterium*** canettii and M. africanum)

II 420839-67-4
 RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
 (gene Senx3, sequence homolog; partial DNA and amino acid sequences of ***Mycobacterium*** genes Senx3 and Regx3, including the Senx3-Regx3 intergenic spacer that contains the ETR-D repeat)

II 1123333-07-2 1123333-10-7 1123333-13-0 1123333-16-3 1123333-19-6
 1123333-22-1 1123333-25-4
 RL: ANT (Analyte); BUU (Biological use, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
 (nucleotide sequence; partial DNA and amino acid sequences of ***Mycobacterium*** genes Senx3 and Regx3, including the Senx3-Regx3 intergenic spacer that contains the ETR-D repeat)

II 1088759-75-4 1088759-77-6 1088759-79-8

RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(nucleotide sequence; partial DNA and amino acid sequences of novel oxyR, ***hsp65*** and mptR genes found in ***Mycobacterium*** canettii and M. africanum)

L9 ANSWER 20 OF 71 CAPLUS COPYRIGHT 2009 ACS ON STN
AN 2008:455470 CAPLUS <<LOGINID:20090617>>
DN 149:324704
TI Construction and expression of eukaryotic expression vector pIHSP65 of
Mycobacterium tuberculosis
AU Li, Yan; Deng, Junxia; Guan, Dawei
CS Department of EMT Center, The Affiliated Provincial Hospital, Anhui
Medical University, Hefei, Anhui Province, 231000, Peop. Rep. China
SO Xinxiang Yixueyuan Xuebao (2007), 24(1), 29-33
CODEN: XYIXEQ; ISSN: 1004-7239
PB Xinxiang Yixueyuan Xuebao Bianji Weiyuanhui
DT Journal
LA Chinese
AB The eukaryotic expression vector based on ***HSP65*** gene of
mycobacterium tuberculosis was constructed. ***HSP65*** gene
was cloned from genome of ***mycobacterium*** tuberculosis H37Rv
strain by PCR, and inserted into multiple cloning site A's corresponding
sites of dicistronic eukaryotic expression vector pIRES to construct
eukaryotic expression vector pIHSP65, then transfected into Hela cell by
using poly-cation. Finally, the expression of ***HSP65*** protein was
detected by immunochem. staining. The length and sequence of the cloned
HSP65 segment were correct. The pos. expression of ***HSP65***
in Hela cell, which had been transfection with recombinant plasmid, was
identified by immunohistochem. method. The successful
construction of eukaryotic expression vector pIHSP65 and effective
expression in Hela cells, lays the foundation for constructing
two-antigens dicistronic eukaryotic expression plasmid and further study
in animal.
TI Construction and expression of eukaryotic expression vector pIHSP65 of
Mycobacterium tuberculosis
AB The eukaryotic expression vector based on ***HSP65*** gene of
mycobacterium tuberculosis was constructed. ***HSP65*** gene
was cloned from genome of ***mycobacterium*** tuberculosis H37Rv
strain by PCR, and inserted into multiple cloning site A's corresponding
sites of dicistronic eukaryotic expression vector pIRES to construct
eukaryotic expression vector pIHSP65, then transfected into Hela cell by
using poly-cation. Finally, the expression of ***HSP65*** protein was
detected by immunochem. staining. The length and sequence of the cloned
HSP65 segment were correct. The pos. expression of ***HSP65***
in Hela cell, which had been transfection with recombinant plasmid, was
identified by immunohistochem. method. The successful
construction of eukaryotic expression vector pIHSP65 and effective
expression in Hela cells, lays the foundation. . .
ST cloning vaccine pIHSP65 ***Mycobacterium*** tuberculosis
IT Gene, microbial
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(***HSP65*** ; construction and expression of eukaryotic expression
vector pIHSP65 of ***Mycobacterium*** tuberculosis)
IT Antibacterial agents
HeLa cell
Molecular cloning

Mycobacterium tuberculosis
Transformation, genetic
Vaccines
(construction and expression of eukaryotic expression vector pIHSP65 of
Mycobacterium tuberculosis)
IT ***Primers*** (nucleic acid)
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(construction and expression of eukaryotic expression vector pIHSP65 of
Mycobacterium tuberculosis)
IT Plasmid vectors
(pIHSP65; construction and expression of eukaryotic expression vector
pIHSP65 of ***Mycobacterium*** tuberculosis)

L9 ANSWER 21 OF 71 CAPLUS COPYRIGHT 2009 ACS on STN
AN 2008:137939 CAPLUS <<LOGINID::20090617>>
DN 148:300601
TI PCR-RFLP analysis (PRA) of non tuberculous ***mycobacteria*** (NTM)
isolated from animal specimens and environment using ***hsp65*** and
rpoB genes
AU Bannaliker, A. S.; Verma, Rishendra
CS Indian Veterinary Research Institute, Uttar Pradesh, 243 122, India
SO Indian Journal of Animal Sciences (2007), 77(12), 1211-1218
CODEN: IJLAA4; ISSN: 0367-8318
PB Indian Council of Agricultural Research
DI Journal
LA English
AB Non tuberculous ***mycobacteria*** (99) comprising 34 isolates from
animal specimens, 57 soil and 8 water samples from animal dwellings were
identified on the basis of growth rate, pigmentation, colony
morphol. and biochem. reactions. Of the 8 species recovered from animal
specimens 4 (M. fortuitum, M. smegmatis, M. chelonae and M. abscessus)
were prevalent in soil while only 2 of these species (M. fortuitum and M.
smegmatis) prevailed in water samples. These isolates along with 13 ref.
strains of ***mycobacteria*** were subjected to polymerase chain
reaction-restriction fragment length polymorphism anal. (PRA) of
hsp65 and rpoB genes. All the isolates generated products of 439
bp and 360 bp in PCR of ***hsp65*** and rpoB genes resp. Restriction
digestion of the product of ***hsp65*** and BstEII and HaeIII and that
of rpoB with MspI and HaeIII in sep. reactions and anal. of digests by
agarose gel electrophoresis revealed RFLP patterns characteristic for most
of the species tested. Out of the 16- ***mycobacterial*** species
evaluated, 13 produced a single PRA pattern, while 3 species generated 2
patterns in both the PRA methods. M. abscessus and M. chelonae were
distinguishable from each other. M. fortuitum isolates were
differentiated into M. fortuitum I and M. fortuitum II, M. avium complex
isolates into M. intracellulare and M. avium, M. kansasii isolates into M.
kansasii I and M. kansasii V and M. gordonae into M. gordonae II and M.
gordonae (new type) by both the methods. Both the PRA methods could not
make a distinction between M. tuberculosis and M. bovis however, PRA with
hsp65 was found better since it yielded relatively large sized
and distinct band.

RE.CNT 27 THERE ARE 27 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

TI PCR-RFLP analysis (PRA) of non tuberculous ***mycobacteria*** (NTM)
isolated from animal specimens and environment using ***hsp65*** and
rpoB genes

AB Non tuberculous ***mycobacteria*** (99) comprising 34 isolates from animal specimens, 57 soil and 8 water samples from animal dwellings were ***identified*** on the basis of growth rate, pigmentation, colony morphol. and biochem. reactions. Of the 8 species recovered from animal specimens. . . of these species (*M. fortuitum* and *M. smegmatis*) prevailed in water samples. These isolates along with 13 ref. strains of ***mycobacteria*** were subjected to polymerase chain reaction-restriction fragment length polymorphism anal. (PRA) of ***hsp65*** and *rpoB* genes. All the isolates generated products of 439 bp and 360 bp in PCR of ***hsp65*** and *rpoB* genes resp. Restriction digestion of the product of ***hsp65*** and *BstEII* and *HaeIII* and that of *rpoB* with *MspI* and *HaeIII* in sep. reactions and anal. of digests by agarose gel electrophoresis revealed RFLP patterns characteristic for most of the species tested. Out of the 16- ***mycobacterial*** species evaluated, 13 produced a single PRA pattern, while 3 species generated 2 patterns in both the PRA methods. M. . . the methods. Both the PRA methods could not make a distinction between *M. tuberculosis* and *M. bovis* however, PRA with ***hsp65*** was found better since it yielded relatively large sized and distinct band.

ST PCR RFLP gene ***hsp65*** nontuberculous ***mycobacteria*** detection discrimination; gene *rpoB* PCR RFLP nontuberculous ***mycobacteria*** detection discrimination; ***Mycobacterium*** prevalence water soil animal tissue PCR RFLP

IT ***Primers*** (nucleic acid)
 RL: ARG (Analytical reagent use); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
 (DNA; ***hsp65*** - and *rpoB*-gene-specific PCR-RFLP anal. for detecting, discriminating and detg. prevalence of non tuberculous ***mycobacteria*** (NTM) isolated from animals, water or soil)

IT ***Mycobacterium*** *avium* (complex; ***hsp65*** - and *rpoB*-gene-specific PCR-RFLP anal. for detecting, discriminating and detg. prevalence of non tuberculous ***mycobacteria*** (NTM) isolated from animals, water or soil)

IT Animal tissue
 Animalia
 Animals
 Mycobacterium *abscessus*
 Mycobacterium *chelonae*
 Mycobacterium *fortuitum*
 Mycobacterium *gordonae*
 Mycobacterium *intracellulare*
 Mycobacterium *kansasii*
 Mycobacterium *smegmatis*
 Polymerase chain reaction
 Restriction fragment length polymorphism
 Soils
 (***hsp65*** - and *rpoB*-gene-specific PCR-RFLP anal. for detecting, discriminating and detg. prevalence of non tuberculous ***mycobacteria*** (NTM) isolated from animals, water or soil)

IT Gene, microbial
 RL: ANT (Analyte); DGN (Diagnostic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
 (***hsp65*** ; ***hsp65*** - and *rpoB*-gene-specific PCR-RFLP anal. for detecting, discriminating and detg. prevalence of non tuberculous ***mycobacteria*** (NTM) isolated from animals, water or soil)

IT DNA

RL: ARG (Analytical reagent use); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
 (***primer*** ; ***hsp65*** - and rpoB-gene-specific PCR-RFLP anal. for detecting, discriminating and detg. prevalence of non tuberculous ***mycobacteria*** (NTM) isolated from animals, water or soil)

IT Gene, microbial
 RL: ANT (Analyte); DGN (Diagnostic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
 (rpoB; ***hsp65*** - and rpoB-gene-specific PCR-RFLP anal. for detecting, discriminating and detg. prevalence of non tuberculous ***mycobacteria*** (NTM) isolated from animals, water or soil)

IT 7732-18-5, Water, analysis
 RL: AMX (Analytical matrix); ANST (Analytical study)
 (***hsp65*** - and rpoB-gene-specific PCR-RFLP anal. for detecting, discriminating and detg. prevalence of non tuberculous ***mycobacteria*** (NTM) isolated from animals, water or soil)

L9 ANSWER 22 OF 71 CAPLUS COPYRIGHT 2009 ACS on STN
 AN 2007:1057364 CAPLUS <<LOGINID::20090617>>
 DN 147:337125

TI Method for differentiating or ***identifying*** ***Mycobacterium*** tuberculosis and non-tuberculous ***mycobacteria*** using ***hsp65*** signature nucleotide sequence

IN Kim, Bum Joon; Kim, Hyun Joo; Park, Hae Joon
 PA Seoul National University Industry Foundation, S. Korea
 SO Repub. Korea, No pp. given
 CODEN: KRXXFC

DT Patent
 LA Korean
 FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	KR 692484	B1	20070313	KR 2005-104871	20051103
PRAI	KR 2005-104871		20051103		

AB A method for ***identifying*** ***Mycobacterium*** tuberculosis and non-tuberculous ***mycobacteria*** is provided to conveniently and accurately differentiate ***Mycobacterial*** species by using each 8 signature nucleotide sequences capable of characterizing ***Mycobacterium*** tuberculosis group and non-tuberculous ***mycobacteria*** group. The method comprises the steps of: (a) amplifying a gene fragment including at least one base selected from the group consisting of bases located at 228th, 243th, 543th, 600th, 705th, and 718-720th from a 5'-terminal of a heat shock protein 65(***HSP65***) consisting of total 1623bp of ***Mycobacterial*** species using a ***primer*** specifically amplifying thereof; (b) analyzing the nucleotide sequence of the amplified gene fragment; and (c) comparing the bases above to ***identify*** non-tuberculous ***mycobacteria*** and ***Mycobacterium*** tuberculosis, where the non-tuberculous ***mycobacteria*** is 228th base of C, 243th base of C, 543th base of C, 600th base of C or T, 705th base of G or 718-720th bases of CAG, and the ***Mycobacterium*** tuberculosis is 228th base of A, 243th base of T, 543th base of T, 600th base of G, 705th base of C or 718-720th bases of GGA. The nucleotide sequence of ***primer*** pair for producing PCR amplification product specific to the non-tuberculous ***mycobacteria*** is described. The differentiation kit for non-tuberculous

mycobacteria and ***Mycobacterium*** tuberculosis comprises a
 primer pairs, and the sequences of the ***primers*** have
 been presented.

TI Method for differentiating or ***identifying*** ***Mycobacterium***
 tuberculosis and non-tuberculous ***mycobacteria*** using
 hsp65 signature nucleotide sequence

AB A method for ***identifying*** ***Mycobacterium*** tuberculosis
 and non-tuberculous ***mycobacteria*** is provided to conveniently and
 accurately differentiate ***Mycobacterial*** species by using each 8
 signature nucleotide sequences capable of characterizing
 Mycobacterium tuberculosis group and non-tuberculous
 mycobacteria group. The method comprises the steps of: (a)
 amplifying a gene fragment including at least one base selected from the.
 . . consisting of bases located at 228th, 243th, 543th, 600th, 705th,
 and 718-720th from a 5'-terminal of a heat shock protein 65(***HSP65***
) consisting of total 1623bp of ***Mycobacterial*** species using a
 primer specifically amplifying thereof; (b) analyzing the
 nucleotide sequence of the amplified gene fragment; and (c) comparing the
 bases above to ***identify*** non-tuberculous ***mycobacteria***
 and ***Mycobacterium*** tuberculosis, where the non-tuberculous
 mycobacteria is 228th base of C, 243th base of C, 543th base of
 C,
 600th base of C or T, 705th base of G or 718-720th bases of CAG, and the
 Mycobacterium tuberculosis is 228th base of A, 243th base of T,
 543th base of T, 600th base of G, 705th base of C or 718-720th bases of
 GGA. The nucleotide sequence of ***primer*** pair for producing PCR
 amplification product specific to the non-tuberculous ***mycobacteria***
 is described. The differentiation kit for non-tuberculous
 mycobacteria and ***Mycobacterium*** tuberculosis comprises a
 primer pairs, and the sequences of the ***primers*** have
 been presented.

ST ***Mycobacterium*** tuberculosis nontuberculous genotyping PCR
 Hsp65 gene

IT Heat-shock proteins
 RL: BSU (Biological study, unclassified); BIOL (Biological study)
 (HSP 65; method for differentiating or ***identifying***
 Mycobacterium tuberculosis and non-tuberculous
 mycobacteria using ***hsp65*** signature nucleotide
 sequence)

IT Gene, microbial
 RL: BSU (Biological study, unclassified); BIOL (Biological study)
 (***hsp65*** ; method for differentiating or ***identifying***
 Mycobacterium tuberculosis and non-tuberculous
 mycobacteria using ***hsp65*** signature nucleotide
 sequence)

IT Genotypes
 Genotyping (method)
 Mycobacterium
 Mycobacterium tuberculosis
 Polymerase chain reaction
 Tuberculosis
 (method for differentiating or ***identifying***
 Mycobacterium tuberculosis and non-tuberculous
 mycobacteria using ***hsp65*** signature nucleotide
 sequence)

IT ***Primers*** (nucleic acid)
 RL: ARG (Analytical reagent use); BSU (Biological study, unclassified);
 ANST (Analytical study); BIOL (Biological study); USES (Uses)
 (method for differentiating or ***identifying***
 Mycobacterium tuberculosis and non-tuberculous
 mycobacteria using ***hsp65*** signature nucleotide
 sequence)

L9 ANSWER 23 OF 71 CAPLUS COPYRIGHT 2009 ACS on STN
 AN 2007:747037 CAPLUS <<LOGINID:20090617>>
 DN 148:4726
 TI Molecular ***identification*** by random amplified polymorphic DNA
 analysis of a pseudo-outbreak of ***Mycobacterium*** fortuitum due to
 cross-contamination of clinical samples
 AU Ortiz, Alberto; Esteban, Jaime; Zamora, Nieves
 CS Department of Clinical Microbiology, Fundacion Jimenez Diaz-UTE, Madrid,
 28040, Spain
 SO Journal of Medical Microbiology (2007), 56(6), 871-872
 CODEN: JMMIAV; ISSN: 0022-2615
 PB Society for General Microbiology
 DT Journal
 LA English
 AB A pseudo-outbreak of ***Mycobacterium*** fortuitum, probably due to
 cross-contamination from a true pos. urine specimen, detected in the lab.
 is described. All specimens sent to the ***mycobacteriol*** lab.
 were decontaminated with N-acetylcysteine-NaOH according to commonly
 accepted protocols. After decontamination, all samples were inoculated
 into MGIT liq. culture medium (BD) and onto Coletsos and Lowenstein-Jensen
 slants (bioMerieux). ***Identification*** of the isolates was
 performed using common biochem. tests and PCR-RFLP anal. of the
 hsp65 gene. Susceptibility testing of the strains was done using
 amikacin, clarithromycin, ciprofloxacin and imipenem E-test strips on
 Muller-Hinton agar plates enriched with 5 % sheep blood incubated at
 37.degree. in a 5% CO2 atmosphere for 3 days. The mol. epidemiol. anal.
 was done by the random amplified polymorphic DNA (RAPD) technique using
 the ***primers*** OPA-2, OPA-18, INS-2 and IS-986FP. Strains were
 considered to be identical when the electrophoretic pattern was the same
 with at least three ***primers*** . Other unrelated M. fortuitum
 strains isolated from clin. samples from our collection were used as
 controls. A NPRGM was recovered in five samples processed on the same
 day. During the inoculation in the culture media, samples were located
 near to each other, and even next to each other in some cases. In three
 samples, the ***mycobacterial*** strain was isolated in the MGIT
 medium, and in another one, only one colony grew on a Coletsos slant
 (bioMerieux).

RE.CNT 10 THERE ARE 10 CITED REFERENCES AVAILABLE FOR THIS RECORD
 ALL CITATIONS AVAILABLE IN THE RE FORMAT

TI Molecular ***identification*** by random amplified polymorphic DNA
 analysis of a pseudo-outbreak of ***Mycobacterium*** fortuitum due to
 cross-contamination of clinical samples
 AB A pseudo-outbreak of ***Mycobacterium*** fortuitum, probably due to
 cross-contamination from a true pos. urine specimen, detected in the lab.
 is described. All specimens sent to the ***mycobacteriol*** lab.
 were decontaminated with N-acetylcysteine-NaOH according to commonly
 accepted protocols. After decontamination, all samples were inoculated
 into MGIT liq. culture medium (BD) and onto Coletsos and Lowenstein-Jensen
 slants (bioMerieux). ***Identification*** of the isolates was

performed using common biochem. tests and PCR-RFLP anal. of the ***hsp65*** gene. Susceptibility testing of the strains was done using amikacin, clarithromycin, ciprofloxacin and imipenem E-test strips on Muller-Hinton agar plates. . . atmosphere for 3 days. The mol. epidemiol. anal. was done by the random amplified polymorphic DNA (RAPD) technique using the ***primers*** OPA-2, OPA-18, INS-2 and IS-986FP. Strains were considered to be identical when the electrophoretic pattern was the same with at least three ***primers***. Other unrelated M. fortuitum strains isolated from clin. samples from our collection were used as controls. A NPRGM was recovered. . . samples were located near to each other, and even next to each other in some cases. In three samples, the ***mycobacterial*** strain was isolated in the MGIT medium, and in another one, only one colony grew on a Coletsos slant (bioMeritux).

ST ***Mycobacterium*** phenotype antibiotic resistance RAPD
 IT Antibiotic resistance
 Human
 Mycobacterium fortuitum
 Phenotypes
 RAPD analysis
 (mol. ***identification*** by random amplified polymorphic DNA anal. of a pseudo-outbreak of ***Mycobacterium*** fortuitum due to cross-contamination of clin. samples)

IT Epidemiology
 (mol.; mol. ***identification*** by random amplified polymorphic DNA anal. of a pseudo-outbreak of ***Mycobacterium*** fortuitum due to cross-contamination of clin. samples)

IT 37517-28-5, Amikacin 64221-86-9, Imipenem 81103-11-9, Clarithromycin 85721-33-1, Ciprofloxacin
 RL: BSU (Biological study, unclassified); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
 (mol. ***identification*** by random amplified polymorphic DNA anal. of a pseudo-outbreak of ***Mycobacterium*** fortuitum due to cross-contamination of clin. samples)

L9 ANSWER 24 OF 71 CAPLUS COPYRIGHT 2009 ACS on STN
 AN 2007:673037 CAPLUS <<LOGINID:20090617>>
 DN 147:90504
 TI Method and kit for detecting the presence or absence of a target cell in a sample
 IN Angles D'Auriac, Marc
 PA Genpoint A/S, Norway; Gardner, Rebecca
 SO PCT Int. Appl., 41pp.
 CODEN: PIXXD2
 DT Patent
 LA English
 FAN.CNT 1

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2007068904	A1	20070621	WO 2006-GB4629	20061212
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BW, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, GT, HN, HR, HU, ID, IL, IN, IS, JP, KE, KG, KM, KN, KP, KR, KZ, LA, LC, LK, LR, LS, LT, LU, LV, LY, MA, MD, MG, MK, MN, MW, MX, MY, MZ, NA, NG, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RS, RU, SC, SD, SE, SG, SK, SL, SM, SV, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, ZA, ZM, ZW				

RW: AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE,
 IS, IT, LT, LU, LV, MC, NL, PL, PT, RO, SE, SI, SK, TR, BF, BJ,
 CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG, BW, GH,
 GM, KE, LS, MW, MZ, NA, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY,
 KG, KZ, MD, RU, TJ, TM
 AU 2006324486 A1 20070621 AU 2006-324486 20061212
 CA 2631877 A1 20070621 CA 2006-2631877 20061212
 EP 1969138 A1 20080917 EP 2006-820489 20061212
 R: AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE,
 IS, IT, LT, LU, LV, MC, NL, PL, PT, RO, SE, SI, SK, TR
 JP 2009518053 T 20090507 JP 2008-545076 20061212
 CN 101374960 A 20090225 CN 2006-80046310 20080610
 PRAI GB 2005-25231 A 20051212
 WO 2006-GB4629 W 20061212
 AB The present invention relates to a method for detecting the presence or
 absence of a target cell in a sample, said method comprising (a) binding
 cells in said sample to a particulate and mixable solid support; (b)
 eluting the cells from the solid support without the use of competitor
 mols. to disrupt the interaction between the cell and the solid support;
 (c) after lysis of said cells, detecting the presence or absence of
 nucleic acid characteristic of said target cell, wherein said solid
 support does not have antibodies or antibody fragments immobilized
 thereon. Kits for carrying out the method of the invention are also
 provided. BUGS'n BEADS BW buffer and magnetic beads were added to urine
 samples and samples were mixed during incubation for 15 min. The beads
 were immobilized to the side of the tubes using a magnetic separator and
 the supernatant was removed. The beads were washed with 70% ethanol in
 water, incubated at 80.degree. for 10 min, and immobilized by magnetic
 sepn. Supernatant was analyzed by PCR amplification for Chlamydia
 trachomatis.
 RE.CNT 6 THERE ARE 6 CITED REFERENCES AVAILABLE FOR THIS RECORD
 ALL CITATIONS AVAILABLE IN THE RE FORMAT
 ST target cell detection binding particulate mixable solid; nucleic acid
 identification particulate sepd target cell; Chlamydia
 trachomatis
 detection urine magnetic bead sepn PCR amplification
 IT Bordetella pertussis
 Chlamydia
 Chlamydia pneumoniae
 Chlamydia trachomatis
 Gram-negative bacteria
 Mollicutes
 Mycobacterium abscessus
 Mycoplasma pneumoniae
 Neisseria gonorrhoeae
 (as cell; method and kit using particulate and mixable solid support
 and detection of nucleic acids for detecting presence or absence of
 target cells in samples)
 IT Plasmids
 (cryptic, PCR ***primers*** for detection of nucleic acid for, of
 Chlamydia trachomatis; method and kit using particulate and mixable
 solid support and detection of nucleic acids for detecting presence or
 absence of target cells in samples)
 IT Gene, microbial
 RL: ARG (Analytical reagent use); BSU (Biological study, unclassified);
 DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL
 (Biological study); USES (Uses)

(**hsp65** , PCR **primers** for detection of nucleic acid for, of **Mycobacterium** abscessus; method and kit using particulate and mixable solid support and detection of nucleic acids for detecting presence or absence of target cells in samples)

IT 942319-58-6 942319-59-7
 RL: ARG (Analytical reagent use); BSU (Biological study, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
 (as PCR **primer** in detection of human respiratory syncytial virus; method and kit using particulate and mixable solid support and detection of nucleic acids for detecting presence or absence of target cells in samples)

IT 942319-54-2
 RL: ARG (Analytical reagent use); BSU (Biological study, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
 (as forward PCR **primer** in detection of Chlamydia trachomatis in urine samples; method and kit using particulate and mixable solid support and detection of nucleic acids for detecting presence or absence of target cells in samples)

IT 942319-56-4
 RL: ARG (Analytical reagent use); BSU (Biological study, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
 (as forward PCR **primer** in detection of **Mycobacterium** abscessus; method and kit using particulate and mixable solid support and detection of nucleic acids for detecting presence or absence of target cells in samples)

IT 942319-55-3
 RL: ARG (Analytical reagent use); BSU (Biological study, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
 (as reverse PCR **primer** in detection of Chlamydia trachomatis in urine samples; method and kit using particulate and mixable solid support and detection of nucleic acids for detecting presence or absence of target cells in samples)

IT 942319-57-5
 RL: ARG (Analytical reagent use); BSU (Biological study, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
 (as reverse PCR **primer** in detection of **Mycobacterium** abscessus; method and kit using particulate and mixable solid support and detection of nucleic acids for detecting presence or absence of target cells in samples)

L9 ANSWER 25 OF 71 CAPLUS COPYRIGHT 2009 ACS on STN
 AN 2006:1304935 CAPLUS <<LOGINID::20090617>>
 DN 146:515458
 TI Differentiation of **mycobacterial** species by **hsp65** duplex PCR followed by duplex-PCR-based restriction analysis and direct sequencing

AU Kim, Hyun-Ju; Mun, Ho-Suk; Kim, Hong; Oh, Eun-Ju; Ha, Youngju; Bai, Gill-Han; Park, Young-Gil; Cha, Chang-Yong; Kook, Yoon-Hoh; Kim, Bum-Joon

CS Department of Microbiology and Immunology, Cancer Research Institute and Liver Research Institute, College of Medicine, Seoul National University, Seoul, 110-799, S. Korea

SO Journal of Clinical Microbiology (2006), 44(11), 3855-3862

CODEN: JCMIDW; ISSN: 0095-1137

PB American Society for Microbiology

DT Journal

LA English

AB Here we describe a novel duplex PCR method which can differentiate
 Mycobacterium tuberculosis and nontuberculosis
 mycobacteria (NTM) strains by amplifying ***hsp65*** DNAs of
 different sizes (195 and 515 bp, resp.). The devised technique was
 applied to 54 ref. and 170 clin. isolates and differentiated all strains
 into their resp. groups with 100% sensitivity and specificity.
 Furthermore, a duplex PCR-restriction anal. (duplex PRA) and a direct
 sequencing protocol were developed to differentiate NTM strains at the
 species and subspecies levels based on previously reported ***hsp65***
 DNA sequences and then applied to 105 NTM clin. isolates. All NTM
 isolates were clearly differentiated at the species and subspecies levels
 by subsequent procedures (PRA or direct sequencing) targeting 515-bp NTM
 duplex PCR amplicons. Our results suggest that novel duplex PCR-based
 methods are sensitive and specific for ***identifying***
 mycobacterial culture isolates at the species level.

RE.CNT 25 THERE ARE 25 CITED REFERENCES AVAILABLE FOR THIS RECORD

ALL CITATIONS AVAILABLE IN THE RE FORMAT

TI Differentiation of ***mycobacterial*** species by ***hsp65***
 duplex PCR followed by duplex-PCR-based restriction analysis and direct
 sequencing

AB Here we describe a novel duplex PCR method which can differentiate
 Mycobacterium tuberculosis and nontuberculosis
 mycobacteria (NTM) strains by amplifying ***hsp65*** DNAs of
 different sizes (195 and 515 bp, resp.). The devised technique was
 applied to 54 ref. and 170 clin. . . a direct sequencing protocol were
 developed to differentiate NTM strains at the species and subspecies
 levels based on previously reported ***hsp65*** DNA sequences and then
 applied to 105 NTM clin. isolates. All NTM isolates were clearly
 differentiated at the species and. . . sequencing) targeting 515-bp NTM
 duplex PCR amplicons. Our results suggest that novel duplex PCR-based
 methods are sensitive and specific for ***identifying***
 mycobacterial culture isolates at the species level.

ST ***Mycobacterium*** species differentiation ***hsp65*** duplex PCR
 restriction analysis sequencing

IT DNA sequence analysis
 Mycobacterium tuberculosis
 Tuberculosis
 (differentiation of ***mycobacterial*** species by ***hsp65***
 duplex PCR followed by duplex-PCR-based restriction anal. and direct
 sequencing)

II ***Primers*** (nucleic acid)
 RI: ARG (Analytical reagent use); DGN (Diagnostic use); PRP (Properties);
 ANST (Analytical study); BIOL (Biological study); USES (Uses)
 (differentiation of ***mycobacterial*** species by ***hsp65***
 duplex PCR followed by duplex-PCR-based restriction anal. and direct
 sequencing)

II Genetic methods
 (duplex-PCR-based restriction anal.; differentiation of
 mycobacterial species by ***hsp65*** duplex PCR followed
 by
 duplex-PCR-based restriction anal. and direct sequencing)

II Polymerase chain reaction
 (duplex; differentiation of ***mycobacterial*** species by

anal. ***hsp65*** duplex PCR followed by duplex-PCR-based restriction
 and direct sequencing)
 IT Gene, microbial
 RL: ANT (Analyte); DGN (Diagnostic use); ANST (Analytical study); BIOL
 (Biological study); USES (Uses)
 (***hsp65*** ; differentiation of ***mycobacterial*** species by
 hsp65 duplex PCR followed by duplex-PCR-based restriction
 anal.
 and direct sequencing)
 IT Human
 (isolates from; differentiation of ***mycobacterial*** species by
 hsp65 duplex PCR followed by duplex-PCR-based restriction
 anal.
 and direct sequencing)
 IT ***Diagnosis***
 (mol.; differentiation of ***mycobacterial*** species by
 hsp65 duplex PCR followed by duplex-PCR-based restriction
 anal.
 and direct sequencing)
 IT ***Mycobacterium***
 (nontuberculosis; differentiation of ***mycobacterial*** species by
 hsp65 duplex PCR followed by duplex-PCR-based restriction
 anal.
 and direct sequencing)
 IT 936858-56-9 936858-57-0 936858-58-1 936858-59-2 936858-60-5
 936858-61-6 936858-62-7 936858-64-9 936858-65-0
 RL: ARG (Analytical reagent use); DGN (Diagnostic use); PRP (Properties);
 ANST (Analytical study); BIOL (Biological study); USES (Uses)
 (***primer*** ; differentiation of ***mycobacterial*** species
 by ***hsp65*** duplex PCR followed by duplex-PCR-based restriction
 anal. and direct sequencing)

L9 ANSWER 26 OF 71 CAPLUS COPYRIGHT 2009 ACS on STN

AN 2006:1013535 CAPLUS <<LOGINID::20090617>>

DN 146:39451

TI Genetic analysis of ***Mycobacterium*** avium complex strains used for
 producing purified protein derivatives

AU Semret, Makeda; Bakker, Douwe; Smart, Nonie; Olsen, Ingrid; Haslow, Kaare;
 Behr, Marcel A.

CS McGill University Health Centre, Montreal, QC, Can.

SO Clinical and Vaccine Immunology (2006), 13(9), 991-996

CODEN: CVILA6; ISSN: 1556-6811

PB American Society for Microbiology

DT Journal

LA English

AB For over a century, purified protein derivs. (PPD) have been used to
 detect ***mycobacterial*** infections in humans and livestock. Among
 these, reagents to detect infections by ***Mycobacterium*** avium
 complex organisms have been produced, but the utility of these reagents
 has not been clearly established due in part to limited biol. and immunol.
 standardization. Because there is little information about the strains
 used to produce these reagents (avian PPD, intracellulare PPD,
 scrofulaceum PPD, and Johnin), we have performed genetic characterizations
 of strains used to produce these products. Sequence anal. of 16S rRNA and
 the ***hsp65*** gene provided results concordant with species
 designations provided for M. avium, ***Mycobacterium***

intracellular, and ***Mycobacterium*** scrofulaceum organisms. For M. avium strains, comparative genomic hybridization was performed on a whole-genome DNA microarray, revealing one novel 7.9-kilobase genomic deletion in certain Johnin-producing strains, in addn. to genomic variability inherent to the particular M. avium subspecies. Our findings indicate that considerable genomic differences exist between organisms used for reagents and the infecting organism being studied. These results serve as a baseline for potency studies of different preps. and should aid in comparative studies of newly discovered antigens for the ***diagnosis*** of infection and disease by M. avium complex organisms.

RE.CNT 47 THERE ARE 47 CITED REFERENCES AVAILABLE FOR THIS RECORD

ALL CITATIONS AVAILABLE IN THE RE FORMAT

TI Genetic analysis of ***Mycobacterium*** avium complex strains used for producing purified protein derivatives

AB For over a century, purified protein derivs. (PPD) have been used to detect ***mycobacterial*** infections in humans and livestock. Among these, reagents to detect infections by ***Mycobacterium*** avium complex organisms have been produced, but the utility of these reagents has not been clearly established due in part. . . Johnin), we have performed genetic characterizations of strains used to produce these products. Sequence anal. of 16S rRNA and the ***hsp65*** gene provided results concordant with species designations provided for M. avium, ***Mycobacterium*** intracellular, and ***Mycobacterium*** scrofulaceum organisms. For M. avium strains, comparative genomic hybridization was performed on a whole-genome DNA microarray, revealing one novel 7.9-kilobase. . . a baseline for potency studies of different preps. and should aid in comparative studies of newly discovered antigens for the ***diagnosis*** of infection and disease by M. avium complex organisms.

ST multiplex PCR ***Mycobacterium*** genotyping purified protein deriv

IT rRNA
 RL: ANT (Analyte); ANST (Analytical study)
 (16 S; PCR anal. of ***Mycobacterium*** avium complex strains used for producing purified protein derivs.)

IT Heat-shock proteins
 RL: ANT (Analyte); ANST (Analytical study)
 (HSP 65, gene ***hsp65*** ; PCR anal. of ***Mycobacterium*** avium complex strains used for producing purified protein derivs.)

IT Genotyping (method)
 Mycobacterium avium
 Mycobacterium intracellular
 Mycobacterium scrofulaceum
 (PCR anal. of ***Mycobacterium*** avium complex strains used for producing purified protein derivs.)

IT ***Primers*** (nucleic acid)
 RL: ARG (Analytical reagent use); PRP (Properties); ANST (Analytical study); USES (Uses)
 (PCR anal. of ***Mycobacterium*** avium complex strains used for producing purified protein derivs.)

IT Mutation
 (deletion, LSPin (large sequence polymorphism); PCR anal. of ***Mycobacterium*** avium complex strains used for producing purified protein derivs.)

purified protein derivs.)

IT Gene, microbial
 RL: ANT (Analyte); ANST (Analytical study)
 (***hsp65*** ; PCR anal. of ***Mycobacterium*** avium complex

strains used for producing purified protein derivs.)

IT Microsatellite DNA
 RL: ANT (Analyte); ANST (Analytical study)
 (locus 1, locus 2, locus 8, locus 9; PCR anal. of ***Mycobacterium***
 avium complex strains used for producing purified protein derivs.)

IT Polymerase chain reaction
 (multiplex; PCR anal. of ***Mycobacterium*** avium complex strains
 used for producing purified protein derivs.)

IT Tuberculin
 RL: BPN (Biosynthetic preparation); BIOL (Biological study); PREP
 (Preparation)
 (purified protein deriv.; PCR anal. of ***Mycobacterium*** avium
 complex strains used for producing purified protein derivs.)

IT 916531-71-0 916531-72-1 916531-73-2 916531-74-3 916531-75-4
 916531-76-5 916531-77-6 916531-78-7 916531-79-8 916531-80-1
 916531-81-2 916531-82-3 916531-83-4 916531-84-5 916531-85-6
 RL: ARG (Analytical reagent use); PRP (Properties); ANST (Analytical
 study); USES (Uses)
 (PCR ***primer*** ; PCR anal. of ***Mycobacterium*** avium
 complex strains used for producing purified protein derivs.)

L9 ANSWER 27 OF 71 CAPLUS COPYRIGHT 2009 ACS on STN

AN 2006:996526 CAPLUS <<LOGINID::20090617>>

DN 145:466501

TI ***Primer*** designing for multiple PCR for detection of
 Mycobacterium tuberculosis strain

IN Fan, Hong; Ying, Binwu; Wang, Lanlan; Wen, Fuqiang

PA West China Hospital, Sichuan University, Peop. Rep. China

SO Faming Zhuanti Shenqing Gongkai Shuomingshu, 21pp.

CODEN: CNXHEV

DT Patent

LA Chinese

FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	CN 1834258	A	20060920	CN 2005-10022138	20051125
	CN 100368559	C	20080213		
PRAI	CN 2005-10022138		20051125		

AB The invention provides a ***primer*** sets for detection of
 Mycobacterium tuberculosis. The method comprises: (1) adding
 non-bacterial genome sequences YB1 and YB2 to 5' end of oligonucleotide
 primer P1 and P2 resp. to obtain specific long ***primers***
 YB1-P1 and YB2-P2 as ***primer*** pairs for the first stage PCR in
 multi-amplification process, and (2) using the YB1 and YB2 as
 primer pairs for the second stage PCR in multi-amplification
 process. The method provided in this invention can be used of
 identification of ***Mycobacterium*** tuberculosis different
 strain.

TI ***Primer*** designing for multiple PCR for detection of
 Mycobacterium tuberculosis strain

AB The invention provides a ***primer*** sets for detection of
 Mycobacterium tuberculosis. The method comprises: (1) adding
 non-bacterial genome sequences YB1 and YB2 to 5' end of oligonucleotide
 primer P1 and P2 resp. to obtain specific long ***primers***
 YB1-P1 and YB2-P2 as ***primer*** pairs for the first stage PCR in
 multi-amplification process, and (2) using the YB1 and YB2 as
 primer pairs for the second stage PCR in multi-amplification

process. The method provided in this invention can be used of
 identification of ***Mycobacterium*** tuberculosis different
 strain.

ST ***Mycobacterium*** tuberculosis strain PCR ***primer***
 IT Gene, microbial
 RL: ANT (Analyte); ANST (Analytical study)
 (IS6110; ***primer*** designing for multiple PCR for detection of
 Mycobacterium tuberculosis strain)

IT Gene, microbial
 RL: ANT (Analyte); BSU (Biological study, unclassified); ANST (Analytical
 study); BIOL (Biological study)
 (for 32kDa protein, amplification of; ***primer*** designing for
 multiple PCR for detection of ***Mycobacterium*** tuberculosis
 strain)

IT Gene, microbial
 RL: ANT (Analyte); ANST (Analytical study)
 (for ***hsp65***; ***primer*** designing for multiple PCR for
 detection of ***Mycobacterium*** tuberculosis strain)

IT Gene, microbial
 RL: ANT (Analyte); ANST (Analytical study)
 (mtp40; ***primer*** designing for multiple PCR for detection of
 Mycobacterium tuberculosis strain)

IT Genetic methods
 Mycobacterium tuberculosis
 PCR (polymerase chain reaction)
 (***primer*** designing for multiple PCR for detection of
 Mycobacterium tuberculosis strain)

IT ***Primers*** (nucleic acid)
 RL: BUU (Biological use, unclassified); PRP (Properties); BIOL (Biological
 study); USES (Uses)
 (***primer*** designing for multiple PCR for detection of
 Mycobacterium tuberculosis strain)

IT 913582-98-6 913582-99-7
 RL: BUU (Biological use, unclassified); PRP (Properties); BIOL (Biological
 study); USES (Uses)
 (nucleotide sequence; ***primer*** designing for multiple PCR for
 detection of ***Mycobacterium*** tuberculosis strain)

IT 913583-10-5, 1: PN: CN1834258 SEQID: 1 unclaimed DNA 913583-11-6, 2: PN:
 CN1834258 SEQID: 2 unclaimed DNA 913583-12-7, 3: PN: CN1834258 SEQID: 3
 unclaimed DNA 913583-13-8, 4: PN: CN1834258 SEQID: 4 unclaimed DNA
 913583-14-9 913583-15-0 913583-16-1 913583-17-2 913583-18-3
 913583-19-4 913583-20-7 913583-21-8 913583-22-9 913583-23-0
 913583-24-1 913583-25-2 913583-26-3 913583-27-4 913583-28-5
 913583-29-6
 RL: PRP (Properties)
 (unclaimed nucleotide sequence; ***primer*** designing for multiple
 PCR for detection of ***Mycobacterium*** tuberculosis strain)

L9 ANSWER 28 OF 71 CAPLUS COPYRIGHT 2009 ACS ON STN
 AN 2006:986878 CAPLUS <<LOGINID:20090617>>
 DN 146:352092
 TI Development of PCR-RFLP for ***identification*** of eight
 mycobacterial species
 AU Li, Xiaojie; Wang, Hongsheng; Wu, Qinxue; Cui, Pangen; Liu, Xunquan
 CS Institute of Dermatology, Chinese Academy of Medical Sciences and Peking
 Union Medical College, Nanjing, 210042, Peop. Rep. China
 SO Zhonghua Pifuke Zazhi (2005), 38(9), 533-535

CODEN: CHFTAJ; ISSN: 0412-4030

PB Zhongguo Yixue Kexueyuan Pifubing Yanjiusuo
 DT Journal
 LA Chinese

AB A PCR-RFLP method for the ***identification*** of eight
 mycobacterial species was developed. PCR was performed targeting
 the gene encoding 65-kDa heat shock protein which was common to all
 mycobacteria. Two restriction enzymes, BstE II and Hae III, were
 used to digest the PCR products, and specific restriction patterns of
 different ***mycobacteria*** were obtained. The specific restriction
 patterns of different ***mycobacteria*** were identical to the data
 previously reported. *M. avium*, *M. intracellulare*, *M. kansasii*, *M.*
tuberculosis, *M. scrofulaceum*, *M. marinum*, *M. fortuitum* and *M. chelonae*
 could be differentiated in one expt. by PCR-RFLP.

TI Development of PCR-RFLP for ***identification*** of eight
 mycobacterial species

AB A PCR-RFLP method for the ***identification*** of eight
 mycobacterial species was developed. PCR was performed targeting
 the gene encoding 65-kDa heat shock protein which was common to all
 mycobacteria. Two restriction enzymes, BstE II and Hae III, were
 used to digest the PCR products, and specific restriction patterns of
 different ***mycobacteria*** were obtained. The specific restriction
 patterns of different ***mycobacteria*** were identical to the data
 previously reported. *M. avium*, *M. intracellulare*, *M. kansasii*, *M.*
tuberculosis, *M. scrofulaceum*, *M. marinum*, *M. . . .*

ST ***Mycobacterium*** heat shock protein 65 PCR RFLP; PCR RFLP detection
 Mycobacterium heat shock protein ***hsp65*** gene

IT Heat-shock proteins
 RL: BSU (Biological study, unclassified); BIOL (Biological study)
 (HSP 65; PCR-RFLP for ***identification*** of ***Mycobacterial***
 species)

IT ***Mycobacterium*** avium
 Mycobacterium chelonae
 Mycobacterium fortuitum
 Mycobacterium intracellulare
 Mycobacterium kansasii
 Mycobacterium marinum
 Mycobacterium scrofulaceum
 Mycobacterium tuberculosis

Polymerase chain reaction
 Restriction fragment length polymorphism
 (PCR-RFLP for ***identification*** of ***Mycobacterial***
 species)

IT Gene, microbial
 RL: ANT (Analyte); ANST (Analytical study)
 (***hsp65*** ; PCR-RFLP for ***identification*** of
 Mycobacterial species)

IT ***Diagnosis***
 (mol.; PCR-RFLP for ***identification*** of ***Mycobacterial***
 species)

IT 930134-85-3 930134-86-4
 RL: ARG (Analytical reagent use); BUU (Biological use, unclassified); DGN
 (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL
 (Biological study); USES (Uses)
 (PCR ***primer*** ; PCR-RFLP for ***identification*** of
 Mycobacterial species)

IT 81295-18-3 93229-61-9, Restriction endonuclease, BstE II

RL: ARG (Analytical reagent use); BUU (Biological use, unclassified); DGN (Diagnostic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)

(PCR-RFLP for ***identification*** of ***Mycobacterial*** species)

L9 ANSWER 29 OF 71 CAPLUS COPYRIGHT 2009 ACS ON STN

AN 2006:517462 CAPLUS <<LOGINID:20090617>>

DN 146:177739

TI Rapid detection and species ***identification*** of
Mycobacterium spp. using real-time PCR and DNA-Microarray

AU Tobler, Nadia E.; Pfunder, Monika; Herzog, Katrin; Frey, Juerg E.;
Altwegg, Martin

CS Institute of Medical Microbiology, University of Zurich, Zurich, CH-8028,
Switz.

SO Journal of Microbiological Methods (2006), 66(1), 116-124

CODEN: JMIMDQ; ISSN: 0167-7012

PB Elsevier B.V.

DT Journal

LA English

AB Infections with ***mycobacteria*** are an important issue in public
health care. Here we present a proof-of-principle' concept for the

identification of 37 different ***Mycobacterium*** species
using 5' exonuclease real-time PCR and DNA microarray based on the region
upstream of the 65 kDa heat shock protein. With our two PCR probes, one
complementary to all ***mycobacteria*** species, the other specific
for the M. tuberculosis complex, 34 species were properly classified by real-time
PCR. After reamplification and hybridization to a DNA microarray, all
species showed a specific pattern. All 10 blindly tested pos. cultures
revealed a pos. real-time PCR signal with the genus probe. After
reamplification and hybridization, six samples could unambiguously be

identified. One sample showed a mixt. of presumably three
species-specific patterns and sequencing the 16S rRNA confirmed the
presence of a mixt. The hybridization results of three specimens could
not be interpreted because the signal to background ratio was not
sufficient. Two samples considered as neg. controls (LAL Reagent Water
(Cambrex) and DNA of Candida albicans) gave neither a genus nor a M.
tuberculosis complex pos. PCR signal. Based on these results we consider our
method to be a promising tool for the rapid ***identification*** of
different ***mycobacteria*** species, with the advantage of possible
identification of mixed infections or contaminations.

RE.CNT 31 THERE ARE 31 CITED REFERENCES AVAILABLE FOR THIS RECORD

ALL CITATIONS AVAILABLE IN THE RE FORMAT

TI Rapid detection and species ***identification*** of

Mycobacterium spp. using real-time PCR and DNA-Microarray

AB Infections with ***mycobacteria*** are an important issue in public
health care. Here we present a proof-of-principle' concept for the

identification of 37 different ***Mycobacterium*** species
using 5' exonuclease real-time PCR and DNA microarray based on the region
upstream of the 65 kDa heat shock protein. With our two PCR probes, one
complementary to all ***mycobacteria*** species, the other specific
for the M. tuberculosis complex, 34 species were properly classified by real-time
PCR. After reamplification and hybridization. . . cultures revealed a
pos. real-time PCR signal with the genus probe. After reamplification and
hybridization, six samples could unambiguously be ***identified***. .
One sample showed a mixt. of presumably three species-specific patterns
and sequencing the 16S rRNA confirmed the presence of a . . .

tbc-complex pos. PCR signal. Based on these results we consider our method to be a promising tool for the rapid ***identification*** of different ***Mycobacteria*** species, with the advantage of possible ***identification*** of mixed infections or contaminations.

ST real time PCR DNA microarray ***HSP65*** ***Mycobacterium*** species ***identification***; ***Mycobacterium*** species ***identification*** detection ***primer*** probe ***HSP65***

IT ***Primers*** (nucleic acid)
 RL: ARG (Analytical reagent use); BUU (Biological use, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
 (DNA, 65kDaf2, 65KDar3 and 65KDar4; description of a two-step procedure (real-time PCR and DNA microarray) for ***identification*** of 37 different ***Mycobacterium*** species based on upstream ***HSP65*** gene sequence)

IT Heat-shock proteins
 RL: BSU (Biological study, unclassified); BIOL (Biological study) (HSP 65, gene for; rapid detection and species ***identification*** of ***Mycobacterium*** spp. using ***HSP65*** gene-specific real-time PCR and DNA microarray technol.)

IT ***Mycobacterium***
 (description of a two-step procedure (real-time PCR and DNA microarray) for ***identification*** of 37 different ***Mycobacterium*** species based on upstream ***HSP65*** gene sequence)

IT DNA microarray technology
 Mycobacterium tuberculosis
 (description of a two-step procedure (real-time PCR and DNA microarray) for ***identification*** of 37 different ***Mycobacterium*** species based on upstream ***HSP65*** gene sequence, including ***Mycobacterium*** tuberculosis)

IT Gene, microbial
 RL: ANT (Analyte); BUU (Biological use, unclassified); DGN (Diagnostic use); ANST (Analytical study); BIOL (Biological study); USES (Uses) (for ***HSP65***, upstream region; description of a two-step procedure (real-time PCR and DNA microarray) for ***identification*** of 37 different ***Mycobacterium*** species based on upstream ***HSP65*** gene sequence)

IT Probes (nucleic acid)
 RL: ARG (Analytical reagent use); BUU (Biological use, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
 (labeled with FAM, Cy3, Dabcyl or BHQ2; description of a two-step procedure (real-time PCR and DNA microarray) for ***identification*** of 37 different ***Mycobacterium*** species based on upstream ***HSP65*** gene sequence)

IT ***Diagnosis***
 (mol.; description of a two-step procedure (real-time PCR and DNA microarray) for ***identification*** of 37 different ***Mycobacterium*** species based on upstream ***HSP65*** gene sequence, including ***Mycobacterium*** tuberculosis)

IT DNA
 RL: ARG (Analytical reagent use); BUU (Biological use, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
 (***primer***, 65kDaf2, 65KDar3 and 65KDar4; description of a two-step procedure (real-time PCR and DNA microarray) for ***identification*** of 37 different ***Mycobacterium*** species

based on upstream ***HSP65*** gene sequence)

IT Polymerase chain reaction
(real-time; rapid detection and species ***identification*** of
Mycobacterium spp. using ***HSP65*** gene-specific
real-time PCR and DNA microarray technol.)

IT 919130-80-6
RL: ARG (Analytical reagent use); BUU (Biological use, unclassified); DGN
(Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL
(Biological study); USES (Uses)
(***primer*** 65kDar3; rapid detection and species
identification of ***Mycobacterium*** spp. using
HSP65 gene-specific real-time PCR and DNA microarray technol.)

IT 919130-79-3
RL: ARG (Analytical reagent use); BUU (Biological use, unclassified); DGN
(Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL
(Biological study); USES (Uses)
(***primer*** 65kDaf2; rapid detection and species
identification of ***Mycobacterium*** spp. using
HSP65 gene-specific real-time PCR and DNA microarray technol.)

IT 919130-81-7
RL: ARG (Analytical reagent use); BUU (Biological use, unclassified); DGN
(Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL
(Biological study); USES (Uses)
(***primer*** 65kDar4; rapid detection and species
identification of ***Mycobacterium*** spp. using
HSP65 gene-specific real-time PCR and DNA microarray technol.)

IT 919130-82-8D, 5'-labeled with FAM and 3'-labeled with Dabcyl
919130-83-9D, 5'-labeled with Cy3 and 3'-labeled with BHQ-2
RL: ARG (Analytical reagent use); BUU (Biological use, unclassified); DGN
(Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL
(Biological study); USES (Uses)
(probe; rapid detection and species ***identification*** of
Mycobacterium spp. using ***HSP65*** gene-specific
real-time PCR and DNA microarray technol.)

IT 6268-49-1D, Dabcyl, oligonucleotide conjugate 76823-03-5D, FAM,
oligonucleotide conjugate 146368-16-3D, Cy3, oligonucleotide conjugate
374591-96-5D, BHQ-2, oligonucleotide conjugate
RL: ARG (Analytical reagent use); BUU (Biological use, unclassified); DGN
(Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL
(Biological study); USES (Uses)
(rapid detection and species ***identification*** of
Mycobacterium spp. using ***HSP65*** gene-specific
real-time PCR and DNA microarray technol.)

L9 ANSWER 30 OF 71 CAPLUS COPYRIGHT 2009 ACS ON STN

AN 2006:450735 CAPLUS <<LOGINID::20090617>>

DN 145:466102

TI Detection of ***Mycobacterium*** avium & M. tuberculosis from human
sputum cultures by PCR-RFLP analysis of ***hsp65*** gene & pncA PCR

AU Bannalikal, A. S.; Verma, Rishendra

CS Mycobacteria Laboratory, Division of Bacteriology & Mycology, Indian
Veterinary Research Institute, Izatnagar, India

SO Indian Journal of Medical Research (2006), 123(2), 165-172

CODEN: IMIREV; ISSN: 0971-5916

PB Indian Council of Medical Research

DT Journal

LA English

AB Background & objectives: ***Identification*** of ***mycobacteria*** by conventional methods is slow, labour intensive and may at times fail to produce precise results. Mol. techniques developed in the recent past, overcome these disadvantages facilitating rapid ***identification*** of most species. We undertook this study to characterize

mycobacteria isolated from sputa of human patients suspected to have tuberculosis by conventional methods and later, by polymerase chain reaction-restriction fragment length polymorphism anal. (PRA) of ***hsp65*** gene and pncA PCR. Methods: Twenty two

mycobacteria isolated from 30 sputum samples were ***identified*** based on growth rate, pigmentation, cultural and biochem. properties and subjected to PRA of ***hsp65*** gene involving amplification of ***hsp65*** gene and digestion of the product with BstEII and HaeIII in sep. reactions and anal. of digests by 3 per cent agarose gel electrophoresis. The ***mycobacteria*** were simultaneously evaluated by M. tuberculosis-specific and M. bovis-specific pncA PCR assays in sep. reactions. Results: With the conventional biochem. tests, the 22 sputum culture isolates were ***identified*** as M. tuberculosis (19) and M. avium complex (MAC) (3). PCR of ***hsp65*** gene yielded 439 bp product in all the ***mycobacteria*** tested. The RFLP patterns of three MAC isolates with BstEII and HaeIII were identical to ref. M. avium strain with two fragments in each of the digest. M. intracellulare ref. strain showed a distinct pattern with 3 fragments each in both enzyme digests. The PRA of ***hsp65*** confirmed MAC isolates as M. avium. M. tuberculosis isolates including H37Rv and M. bovis strains could not be discriminated by PRA of ***hsp65***. The two pncA PCR assays (M. bovis-specific and M. tuberculosis-specific) detected specifically the resp. organisms with an amplification product of 185 bp. The MAC strains yielded no amplification product in both the pncA PCR assays. Interpretation & conclusion: PRA profiles of ***hsp65*** could differentiate MAC isolates into M. avium and M. intracellulare but could not distinguish between M. tuberculosis and M. bovis. PncA PCR assays were found specific in detecting the resp. ***mycobacterial*** species. The study confirms utility of pncA PCR assays in differential ***identification*** of M. tuberculosis and M. bovis and that of PRA of ***hsp65*** in the ***identification*** of M. avium.

RE.CNT 23 THERE ARE 23 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

TI Detection of ***Mycobacterium*** avium & M. tuberculosis from human sputum cultures by PCR-RFLP analysis of ***hsp65*** gene & pncA PCR

AB Background & objectives: ***Identification*** of ***mycobacteria*** by conventional methods is slow, labour intensive and may at times fail to produce precise results. Mol. techniques developed in the recent past, overcome these disadvantages facilitating rapid ***identification*** of most species. We undertook this study to characterize

mycobacteria isolated from sputa of human patients suspected to have tuberculosis by conventional methods and later, by polymerase chain reaction-restriction fragment length polymorphism anal. (PRA) of ***hsp65*** gene and pncA PCR. Methods: Twenty two

mycobacteria isolated from 30 sputum samples were ***identified*** based on growth rate, pigmentation, cultural and biochem. properties and subjected to PRA of ***hsp65*** gene involving amplification of ***hsp65*** gene and digestion of the product with BstEII and HaeIII in sep. reactions and anal. of digests by 3 per cent agarose gel electrophoresis. The ***mycobacteria*** were simultaneously evaluated by M.

tuberculosis-specific and *M. bovis*-specific *pncA* PCR assays in sep. reactions. Results: With the conventional biochem. tests, the 22 sputum culture isolates were ***identified*** as *M. tuberculosis* (19) and *M. avium* complex (MAC) (3). PCR of ***hsp65*** gene yielded 439 bp product in all the ***mycobacteria*** tested. The RFLP patterns of three MAC isolates with BstEII and HaeIII were identical to ref. *M. avium* strain with. . . digest. *M. intracellulare* ref. strain showed a distinct pattern with 3 fragments each in both enzyme digests. The PRA of ***hsp65*** confirmed MAC isolates as *M. avium*. *M. tuberculosis* isolates including H37Rv and *M. bovis* strains could not be discriminated by PRA of ***hsp65***. The two *pncA* PCR assays (*M. bovis*-specific and *M. tuberculosis*-specific) detected specifically the resp. organisms with an amplification product of. . . bp. The MAC strains yielded no amplification product in both the *pncA* PCR assays. Interpretation & conclusion: PRA profiles of ***hsp65*** could differentiate MAC isolates into *M. avium* and *M. intracellulare* but could not distinguish between *M. tuberculosis* and *M. bovis*. *pncA* PCR assays were found specific in detecting the resp. ***mycobacterial*** species. The study confirms utility of *pncA* PCR assays in differential ***identification*** of *M. tuberculosis* and *M. bovis* and that of PRA of ***hsp65*** in the ***identification*** of *M. avium*.

- ST PCR RFLP ***Mycobacterium*** tuberculosis ***diagnosis***
 hsp65 *pncA*
- IT Sputum
 (anal. sample; detection of ***Mycobacterium*** *avium* and *M. tuberculosis* from human sputum cultures by PCR-RFLP anal. of
 hsp65 gene & *pncA* PCR)
- IT Human
 PCR (polymerase chain reaction)
 RFLP (restriction fragment length polymorphism)
 (detection of ***Mycobacterium*** *avium* and *M. tuberculosis* from human sputum cultures by PCR-RFLP anal. of ***hsp65*** gene & *pncA* PCR)
- IT ***Primers*** (nucleic acid)
 RL: ARG (Analytical reagent use); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
 (detection of ***Mycobacterium*** *avium* and *M. tuberculosis* from human sputum cultures by PCR-RFLP anal. of ***hsp65*** gene & *pncA* PCR)
- IT Tuberculosis
 (***diagnosis*** ; detection of ***Mycobacterium*** *avium* and *M. tuberculosis* from human sputum cultures by PCR-RFLP anal. of
 hsp65 gene & *pncA* PCR)
- IT Genotyping (method)
 (discrimination between ***Mycobacterium*** species; detection of
 Mycobacterium *avium* and *M. tuberculosis* from human sputum cultures by PCR-RFLP anal. of ***hsp65*** gene & *pncA* PCR)
- IT Alleles
 (gene *pncA*, detection of; detection of ***Mycobacterium*** *avium* and *M. tuberculosis* from human sputum cultures by PCR-RFLP anal. of
 hsp65 gene & *pncA* PCR)
- IT Gene, microbial
 RL: ANT (Analyte); DGN (Diagnostic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
 (***hsp65*** ; detection of ***Mycobacterium*** *avium* and *M. tuberculosis* from human sputum cultures by PCR-RFLP anal. of
 hsp65 gene & *pncA* PCR)

IT ***Diagnosis***
(mol.; detection of ***Mycobacterium*** avium and M. tuberculosis from human sputum cultures by PCR-RFLP anal. of ***hsp65*** gene & pncA PCR)

IT Gene, microbial
RL: ANT (Analyte); DGN (Diagnostic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(pncA; detection of ***Mycobacterium*** avium and M. tuberculosis from human sputum cultures by PCR-RFLP anal. of ***hsp65*** gene & pncA PCR)

IT ***Diagnosis***
(tuberculosis; detection of ***Mycobacterium*** avium and M. tuberculosis from human sputum cultures by PCR-RFLP anal. of ***hsp65*** gene & pncA PCR)

IT 913767-99-4 913768-00-0 913768-01-1 913768-02-2 913768-03-3
RL: ARG (Analytical reagent use); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(PCR ***primer***; detection of ***Mycobacterium*** avium and M. tuberculosis from human sputum cultures by PCR-RFLP anal. of ***hsp65*** gene & pncA PCR)

IT 81295-18-3 93229-61-9, Restriction endonuclease BstEII
RL: ARG (Analytical reagent use); DGN (Diagnostic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(detection of ***Mycobacterium*** avium and M. tuberculosis from human sputum cultures by PCR-RFLP anal. of ***hsp65*** gene & pncA PCR)

L9 ANSWER 31 OF 71 CAPLUS COPYRIGHT 2009 ACS on STN
AN 2006:329492 CAPLUS <<LOGINID::20090617>>
DN 145:370383
TI Application of four molecular typing methods for analysis of
Mycobacterium fortuitum group strains causing post-mammaplasty infections

AU Sampaio, J. L. M.; Chimara, E.; Ferrazoli, L.; da Silva Telles, M. A.; Del Guercio, V. M. F.; Jerico, Z. V. N.; Miyashiro, K.; Fortaleza, C. M. C. B.; Padoveze, M. C.; Leao, S. C.

CS Departamento de Microbiologia, Imunologia e Parasitologia, Universidade Federal de Sao Paulo, Sao Paulo, Brazil

SO Clinical Microbiology and Infection (2006), 12(2), 142-149
CODEN: CMINFM; ISSN: 1198-743X

PB Blackwell Publishing Ltd.
DT Journal
LA English
AB A cluster of cases of post-augmentation mammaplasty surgical site infections occurred between 2002 and 2004 in Campinas, in the southern region of Brazil. Rapidly growing ***mycobacteria*** were isolated from samples from 12 patients. Eleven isolates were ***identified*** as ***Mycobacterium*** fortuitum and one as ***Mycobacterium*** porcinum by PCR-restriction digestion of the ***hsp65*** gene. These 12 isolates, plus six addnl. M. fortuitum isolates from non-related patients, were typed by pulsed-field gel electrophoresis (PFGE) and three PCR-based techniques: 16S-23S rRNA internal transcribed spacer (ITS) genotyping; randomly amplified polymorphic DNA (RAPD) PCR; and enterobacterial repetitive intergenic consensus (ERIC) PCR. Four novel M. fortuitum allelic variants were ***identified*** by restriction anal. of the ITS fragment. One major cluster, comprising six M. fortuitum isolates, and a second cluster of two isolates, were ***identified***

by the four methods. RAPD-PCR and ITS genotyping were less discriminative than ERIC-PCR. ERIC-PCR was comparable to PFGE as a valuable complementary tool for investigation of this type of outbreak.

RE.CNT 26 THERE ARE 26 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

TI Application of four molecular typing methods for analysis of
Mycobacterium fortuitum group strains causing post-mammaplasty infections

AB . . . post-augmentation mammaplasty surgical site infections occurred between 2002 and 2004 in Campinas, in the southern region of Brazil. Rapidly growing ***mycobacteria*** were isolated from samples from 12 patients. Eleven isolates were ***identified*** as ***Mycobacterium*** fortuitum and one as ***Mycobacterium*** porcinum by PCR-restriction digestion of the ***hsp65*** gene. These 12 isolates, plus six addnl. M. fortuitum isolates from non-related patients, were typed by pulsed-field gel electrophoresis (PFGE). . . randomly amplified polymorphic DNA (RAPD) PCR; and enterobacterial repetitive intergenic consensus (ERIC) PCR. Four novel M. fortuitum allelic variants were ***identified*** by restriction anal. of the ITS fragment. One major cluster, comprising six M. fortuitum isolates, and a second cluster of two isolates, were ***identified*** by the four methods. RAPD-PCR and ITS genotyping were less discriminative than ERIC-PCR. ERIC-PCR was comparable to PFGE as a . . .

ST ***Mycobacterium*** post mammaplasty infection isolate analysis PCR
PFGE; human post mammaplasty infection ***Mycobacterium*** species
identification ***hsp65*** PCR; PCR PFGE comparison
Mycobacterium analysis post mammaplasty infection

IT RAPD analysis
(-PCR; comparison of four mol. typing methods (PFGE, ITS-PCR, RAPD-PCR and ERIC-PCR) for anal. of ***Mycobacterium*** fortuitum group strains causing post-mammaplasty infections in Campinas and other locations)

IT ***Primers*** (nucleic acid)
RL: ARG (Analytical reagent use); BUU (Biological use, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(DNA; comparison of four mol. typing methods (PFGE, ITS-PCR, RAPD-PCR and ERIC-PCR) for anal. of ***Mycobacterium*** fortuitum group strains causing post-mammaplasty infections in Campinas and other locations)

IT Repetitive DNA
RL: ANI (Analyte); BUU (Biological use, unclassified); DGN (Diagnostic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(ERIC (enterobacterial repetitive intergenic consensus); comparison of four mol. typing methods (PFGE, ITS-PCR, RAPD-PCR and ERIC-PCR) for anal. of ***Mycobacterium*** fortuitum group strains causing post-mammaplasty infections)

IT Genetic element
RL: ANI (Analyte); BUU (Biological use, unclassified); DGN (Diagnostic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(ITS (internal transcribed spacer); comparison of four mol. typing methods (PFGE, ITS-PCR, RAPD-PCR and ERIC-PCR) for anal. of ***Mycobacterium*** fortuitum group strains causing post-mammaplasty infections in Campinas and other locations)

IT PCR (polymerase chain reaction)
(ITS-, RAPD- and ERIC-; comparison of four mol. typing methods (PFGE, ITS-PCR, RAPD-PCR and ERIC-PCR) for anal. of ***Mycobacterium***

fortuitum group strains causing post-mammoplasty infections in Campinas and other locations)

IT ***Mycobacterium*** fortuitum
 Mycobacterium porcinum
 (***Mycobacterium*** species ***identification*** of isolates obtained from 12 patients with post-mammoplasty infections in Campinas, including ***Mycobacterium*** fortuitum and M. porcinum)

IT Mammary gland
 (augmentation of, mammoplasty; comparison of four mol. typing methods (PFGE, ITS-PCR, RAPD-PCR and ERIC-PCR) for anal. of
 Mycobacterium fortuitum group strains causing post-mammoplasty infections in Campinas and other locations)

IT Human
 (comparison of four mol. typing methods (PFGE, ITS-PCR, RAPD-PCR and ERIC-PCR) for anal. of ***Mycobacterium*** fortuitum group strains causing post-mammoplasty infections in Campinas)

IT Population genetics
 (comparison of four mol. typing methods (PFGE, ITS-PCR, RAPD-PCR and ERIC-PCR) for anal. of ***Mycobacterium*** fortuitum group strains causing post-mammoplasty infections in Campinas and other locations)

IT Gene, microbial
 RL: ANT (Analyte); BUU (Biological use, unclassified); DGN (Diagnostic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
 (***hsp65*** ; ***Mycobacterium*** species
 identification of isolates obtained from patients with post-mammoplasty infections in Campinas using ***hsp65***
 gene-specific PCR-restriction digestion anal.)

IT Evolution
 (mol.; comparison of four mol. typing methods (PFGE, ITS-PCR, RAPD-PCR and ERIC-PCR) for anal. of ***Mycobacterium*** fortuitum group strains causing post-mammoplasty infections in Campinas and other locations)

IT Surgery
 (plastic, augmentation mammoplasty; comparison of four mol. typing methods (PFGE, ITS-PCR, RAPD-PCR and ERIC-PCR) for anal. of
 Mycobacterium fortuitum group strains causing post-mammoplasty infections in Campinas and other locations)

IT DNA
 RL: ARG (Analytical reagent use); BUU (Biological use, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
 (***primer*** ; comparison of four mol. typing methods (PFGE, ITS-PCR, RAPD-PCR and ERIC-PCR) for anal. of ***Mycobacterium*** fortuitum group strains causing post-mammoplasty infections in Campinas and other locations)

IT Gel electrophoresis
 (pulsed-field; comparison of four mol. typing methods (PFGE, ITS-PCR, RAPD-PCR and ERIC-PCR) for anal. of ***Mycobacterium*** fortuitum group strains causing post-mammoplasty infections in Campinas and other locations)

L9 ANSWER 32 OF 71 CAPLUS COPYRIGHT 2009 ACS ON STN
 AN 2006:158391 CAPLUS <<LOGINID::20090617>>
 DN 145:263808
 TI ***Identification*** of ***Mycobacterium*** marinum 65 kD heat shock protein gene by polymerase chain reaction restriction analysis from lesions of swimming pool granuloma

AU Cai, Lin; Xue, Chen; Zhao, Ting; Ding, Bei-chuan; Zhang, Jian-zhong
CS Department of Dermatology, Peking University People's Hospital, Beijing,
100044, Peop. Rep. China
SO Chinese Medical Journal (Beijing, China, English Edition) (2006), 119(1),
43-48

CODEN: CMJODS; ISSN: 0366-6999

PB Chinese Medical Association

DT Journal

LA English

AB Nontuberculous ***mycobacterium*** (NTM) had been reported to cause cutaneous infections which are difficult to interpret due to the variability of the clin. manifestations. Among NTM infections, ***Mycobacterium*** marinum (M. marinum) are mostly seen to cause skin infection. It is therefore important to establish a rapid approach for detection and ***identification*** of M. marinum from lesions of patients with suspected M. marinum infections. Specimens were obtained from 5 patients with swimming pool granuloma. DNA was extd. and polymerase chain reaction (PCR) was performed. PCR products were digested with Hae III and BstE II, then analyzed by pattern restriction anal. to detect heat shock protein (hsp) 65 kD gene. The 65 kD hsp gene was found in all specimens from patients with swimming pool granuloma. PCR restriction anal. (PRA) ***identified*** all 5 samples to be M. marinum infections, and the result was consistent with that of routine bacteriol. ***identification***. The lesions subsided or markedly improved upon treatment. The authors conclude that PRA is a sensitive, specific and rapid method in ***identification*** of ***mycobacteria***. Application of this method will be helpful for early ***diagnosis*** of ***mycobacterial*** skin infections.

RE.CNT 25 THERE ARE 25 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

TI ***Identification*** of ***Mycobacterium*** marinum 65 kD heat shock protein gene by polymerase chain reaction restriction analysis from lesions of swimming pool granuloma

AB Nontuberculous ***mycobacterium*** (NTM) had been reported to cause cutaneous infections which are difficult to interpret due to the variability of the clin. manifestations. Among NTM infections, ***Mycobacterium*** marinum (M. marinum) are mostly seen to cause skin infection. It is therefore important to establish a rapid approach for detection and ***identification*** of M. marinum from lesions of patients with suspected M. marinum infections. Specimens were obtained from 5 patients with swimming. . . The 65 kD hsp gene was found in all specimens from patients with swimming pool granuloma. PCR restriction anal. (PRA) ***identified*** all 5 samples to be M. marinum infections, and the result was consistent with that of routine bacteriol. ***identification***. The lesions subsided or markedly improved upon treatment. The authors conclude that PRA is a sensitive, specific and rapid method in ***identification*** of ***mycobacteria***. Application of this method will be helpful for early ***diagnosis*** of ***mycobacterial*** skin infections.

ST gene ***hsp65*** specific PCR ***Mycobacterium*** detection human granuloma; PCR restriction enzyme analysis ***hsp65*** specific ***Mycobacterium*** detection

IT PCR (polymerase chain reaction)
(-restriction enzyme anal.; gene ***hsp65*** -specific PCR followed by restriction enzyme anal. (PRA) used to ***identify*** ***Mycobacterium*** marinum in lesions from patients with swimming pool granuloma)

IT ***Primers*** (nucleic acid)
 RL: ARG (Analytical reagent use); DGN (Diagnostic use); PRP (Properties);
 ANST (Analytical study); BIOL (Biological study); USES (Uses)
 (DNA, Tbl1 and Tbl2; gene ***hsp65*** -specific PCR followed by
 restriction enzyme anal. (PRA) used to ***identify***
 Mycobacterium marinum in lesions from patients with swimming
 pool granuloma)

IT Human
 Mycobacterium marinum
 (gene ***hsp65*** -specific PCR followed by restriction enzyme anal.
 (PRA) used to ***identify*** ***Mycobacterium*** marinum in
 lesions from patients with swimming pool granuloma)

IT Gene, microbial
 RL: ANT (Analyte); DGN (Diagnostic use); ANST (Analytical study); BIOL
 (Biological study); USES (Uses)
 (***hsp65*** ; gene ***hsp65*** -specific PCR followed by
 restriction enzyme anal. (PRA) used to ***identify***
 Mycobacterium marinum in lesions from patients with swimming
 pool granuloma)

IT Skin, disease
 (lesion; gene ***hsp65*** -specific PCR followed by restriction
 enzyme anal. (PRA) used to ***identify*** ***Mycobacterium***
 marinum in lesions from patients with swimming pool granuloma)

IT ***Diagnosis***
 (mol.; gene ***hsp65*** -specific PCR followed by restriction enzyme
 anal. (PRA) used to ***identify*** ***Mycobacterium*** marinum
 in lesions from patients with swimming pool granuloma)

IT DNA
 RL: ARG (Analytical reagent use); DGN (Diagnostic use); PRP (Properties);
 ANST (Analytical study); BIOL (Biological study); USES (Uses)
 (***primer*** , Tbl1 and Tbl2; gene ***hsp65*** -specific PCR
 followed by restriction enzyme anal. (PRA) used to ***identify***
 Mycobacterium marinum in lesions from patients with swimming
 pool granuloma)

IT Granuloma
 (swimming pool; gene ***hsp65*** -specific PCR followed by
 restriction enzyme anal. (PRA) used to ***identify***
 Mycobacterium marinum in lesions from patients with swimming
 pool granuloma)

L9 ANSWER 33 OF 71 CAPLUS COPYRIGHT 2009 ACS on STN

AN 2005:620828 CAPLUS <<LOGINID:20090617>>

DN 144:206426

TI PCR restriction fragment length polymorphism analysis (PRA)-algorithm
 targeting 644 bp Heat Shock Protein 65 (***hsp65***) gene for
 differentiation of ***Mycobacterium*** spp.

AU Kim, Hong; Kim, Sun-Hyun; Shim, Tae-Sun; Kim, Mi-na; Bai, Gill-Han; Park,
 Young-Gil; Lee, Sueng-Hyun; Cha, Chang-Yong; Kook, Yoon-Hoh; Kim, Bum-Joon

CS Department of Microbiology and Liver Research Institute, College of
 Medicine, Seoul National University Chongno-gu, 28 Yongon-dong,
 Chongno-gu, Seoul, 110-799, S. Korea

SO Journal of Microbiological Methods (2005), 62(2), 199-209
 CODEN: JMIQDQ; ISSN: 0167-7012

PB Elsevier B.V.

DT Journal

LA English

AB A method based on PCR-restriction fragment length polymorphism anal. (PRA)

using a novel region of the ***hsp65*** gene was developed for the rapid and exact ***identification*** of ***mycobacteria*** to the species level. A 644 bp region of ***hsp65*** in 62 ***mycobacteria*** ref. strains, and 4 related bacterial strains was amplified, and the amplified DNAs were subsequently digested with restriction enzymes, namely, *Ava*II, *Hph*I, and *Hpa*II. Most of the ***mycobacteria*** species were easily differentiated at the species level by the developed method. In particular, the method enabled the sepn. of *M. avium*, *M. intracellulare* and *M. tuberculosis* to the species level by *Ava*II digestion alone. An algorithm was constructed based on the results and a blind test was successfully performed on 251 clin. isolates, which had been characterized by conventional biochem. testing. Our results suggest that this novel PRA offers a simple, rapid, and accurate method for the ***identification*** of ***mycobacteria*** culture isolates at the species level.

RE.CNT 24 THERE ARE 24 CITED REFERENCES AVAILABLE FOR THIS RECORD

ALL CITATIONS AVAILABLE IN THE RE FORMAT

- TI PCR restriction fragment length polymorphism analysis (PRA)-algorithm targeting 644 bp Heat Shock Protein 65 (***hsp65***) gene for differentiation of ***Mycobacterium*** spp.
- AB A method based on PCR-restriction fragment length polymorphism anal. (PRA) using a novel region of the ***hsp65*** gene was developed for the rapid and exact ***identification*** of ***mycobacteria*** to the species level. A 644 bp region of ***hsp65*** in 62 ***mycobacteria*** ref. strains, and 4 related bacterial strains was amplified, and the amplified DNAs were subsequently digested with restriction enzymes, namely, *Ava*II, *Hph*I, and *Hpa*II. Most of the ***mycobacteria*** species were easily differentiated at the species level by the developed method. In particular, the method enabled the sepn. of . . . by conventional biochem. testing. Our results suggest that this novel PRA offers a simple, rapid, and accurate method for the ***identification*** of ***mycobacteria*** culture isolates at the species level.
- ST PCR RFLP algorithm ***hsp65*** gene restriction endonuclease ***Mycobacterium***
- IT Heat-shock proteins
 RL: ANT (Analyte); BSU (Biological study, unclassified); ANST (Analytical study); BIOL (Biological study)
 (HSP 65; PCR RFLP algorithm, targeting ***hsp65*** gene, for ***identification*** of ***Mycobacterium*** in clin. isolates)
- IT Algorithm
 Human
 Mycobacterium
 Mycobacterium *avium*
 Mycobacterium *intracellulare*
 Mycobacterium *tuberculosis*
 PCR (polymerase chain reaction)
 RFLP (restriction fragment length polymorphism)
 (PCR RFLP algorithm, targeting ***hsp65*** gene, for ***identification*** of ***Mycobacterium*** in clin. isolates)
- II ***Primers*** (nucleic acid)
 RL: ARG (Analytical reagent use); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
 (PCR; PCR RFLP algorithm, targeting ***hsp65*** gene, for ***identification*** of ***Mycobacterium*** in clin. isolates)
- IT 81295-07-0, Restriction endonuclease *Ava*II 81295-25-2, Restriction endonuclease *Hpa*II 81295-26-3, Restriction endonuclease *Hph*I

RL: BSU (Biological study, unclassified); DGN (Diagnostic use); BIOL
 (Biological study); USES (Uses)
 (PCR RFLP algorithm, targeting ***hsp65*** gene, for
 identification of ***Mycobacterium*** in clin. isolates)

IT 875804-98-1
 RL: ARG (Analytical reagent use); DGN (Diagnostic use); PRP (Properties);
 ANST (Analytical study); BIOL (Biological study); USES (Uses)
 (PCR ***primer*** HSPF3; PCR RFLP algorithm, targeting
 hsp65 gene, for ***identification*** of
 Mycobacterium in clin. isolates)

IT 875804-99-2
 RL: ARG (Analytical reagent use); DGN (Diagnostic use); PRP (Properties);
 ANST (Analytical study); BIOL (Biological study); USES (Uses)
 (PCR ***primer*** HSPR4; PCR RFLP algorithm, targeting
 hsp65 gene, for ***identification*** of
 Mycobacterium in clin. isolates)

L9 ANSWER 34 OF 71 CAPLUS COPYRIGHT 2009 ACS on STN
 AN 2005:224080 CAPLUS <<LOGINID:20090617>>
 DN 143:279951

TI Comparative evaluation of polymerase chain reaction and restriction enzyme
 analysis: Two amplified targets, ***hsp65*** and rpoB, for
 identification of cultured ***mycobacteria***

AU Cheunoy, Wattana; Prammananan, Therdsak; Chaiprasert, Angkana; Foongladda,
 Suporn

CS Department of Microbiology, Faculty of Medicine, Siriraj Hospital, Mahidol
 University, Bangkok, 10700, Thailand

SO Diagnostic Microbiology and Infectious Disease (2005), 51(3), 165-171
 CODEN: DMIDDZ; ISSN: 0732-8893

PB Elsevier Inc.
 DT Journal
 LA English

AB The increasing incidence of tuberculosis and other ***mycobacterial***
 infections due to AIDS epidemic resulted in the need of rapid and accurate
 identification of isolated ***mycobacteria***. The correct
 identification result leads to the selection of an appropriate
 therapeutic regimen. Polymerase chain reaction and restriction enzyme
 anal. (PCR-REA) has been developed since 1992 and used as the rapid method
 for ***identifying*** ***mycobacteria***. Several genes or
 sequences have been used as an amplified target for PCR-REA. The present
 study aims to evaluate the potential use of PCR-REA of gene-encoding heat
 shock protein 65 kDa (***hsp65***) and .beta.-subunit RNA polymerase
 (rpoB) for the ***identification*** of ***mycobacteria*** compared
 with conventional biochem. ***identification***. Two hundreds clin.
 isolates, consisting of 50 isolates of ***Mycobacterium***
 tuberculosis and 150 isolates of nontuberculous ***mycobacteria***
 (NTM), were submitted for ***identification*** using PCR-REA and
 biochem. method. The results demonstrated that PCR-REA ***identified***
 188 isolates of both M. tuberculosis and NTM concordantly with biochem.
 identification. Discordant ***identification*** results
 obtained from 12 isolates, comprised of 8 M. scrofulaceum, 1 M. avium
 complex, 1 M. malmoense, 1 M. terrae complex, and 1 M. chelonae/abscessus.
 Overall, the concordant percentage of results obtained from PCR-REA
 compared with biochem. method was 100%, 98.8%, and 83.3% for M.
 tuberculosis complex, rapidly growing, and slowly growing
 mycobacteria, resp., and the results of ***hsp65*** PCR-REA
 was in agreement with those obtained from rpoB PCR-REA. From this study,

PCR-REA appears to be a simple, rapid, and reliable method for
 identifying **mycobacteria*** in a routine microbiol. lab.

RE.CNT 31 THERE ARE 31 CITED REFERENCES AVAILABLE FOR THIS RECORD
 ALL CITATIONS AVAILABLE IN THE RE FORMAT

TI Comparative evaluation of polymerase chain reaction and restriction enzyme
 analysis: Two amplified targets, ***hsp65*** and rpoB, for
 identification of cultured ***mycobacteria***

AB The increasing incidence of tuberculosis and other ***mycobacterial***
 infections due to AIDS epidemic resulted in the need of rapid and accurate
 identification of isolated ***mycobacteria***. The correct
 identification result leads to the selection of an appropriate
 therapeutic regimen. Polymerase chain reaction and restriction enzyme
 anal. (PCR-REA) has been developed since 1992 and used as the rapid method
 for ***identifying*** **mycobacteria***. Several genes or
 sequences have been used as an amplified target for PCR-REA. The present
 study aims to evaluate the potential use of PCR-REA of gene-encoding heat
 shock protein 65 kDa (***hsp65***) and .beta.-subunit RNA polymerase
 (rpoB) for the ***identification*** of ***mycobacteria*** compared
 with conventional biochem. ***identification***. Two hundreds clin.
 isolates, consisting of 50 isolates of ***Mycobacterium***
 tuberculosis and 150 isolates of nontuberculous ***mycobacteria***
 (NTM), were submitted for ***identification*** using PCR-REA and
 biochem. method. The results demonstrated that PCR-REA ***identified***
 188 isolates of both M. tuberculosis and NTM concordantly with biochem.
 identification. Discordant ***identification*** results
 obtained from 12 isolates, comprised of 8 M. scrofulaceum, 1 M. avium
 complex, 1 M. malmoense, 1 M. terrae. . . from PCR-REA compared with
 biochem. method was 100%, 98.8%, and 83.3% for M. tuberculosis complex,
 rapidly growing, and slowly growing ***mycobacteria***, resp., and the
 results of ***hsp65*** PCR-REA was in agreement with those obtained
 from rpoB PCR-REA. From this study, PCR-REA appears to be a simple,
 rapid, and reliable method for ***identifying*** **mycobacteria***
 in a routine microbiol. lab.

ST PCR RFLP ***identification*** **Mycobacterium*** human infection

IT RFLP (restriction fragment length polymorphism)
 (PCR; comparative evaluation of polymerase chain reaction and
 restriction enzyme anal. using two amplified targets, ***hsp65***
 and rpoB, for ***identification*** of cultured ***mycobacteria***
)

IT ***Mycobacterium*** abscessus
 Mycobacterium avium
 Mycobacterium malmoense
 Mycobacterium scrofulaceum
 Mycobacterium terrae
 Mycobacterium tuberculosis
 (comparative evaluation of polymerase chain reaction and restriction
 enzyme analysis using two amplified targets, ***hsp65*** and rpoB,
 for ***identification*** of cultured ***mycobacteria***)

IT ***Primers*** (nucleic acid)
 RL: ARG (Analytical reagent use); BUU (Biological use, unclassified); DGN
 (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL
 (Biological study); USES (Uses)
 (comparative evaluation of polymerase chain reaction and restriction
 enzyme analysis using two amplified targets, ***hsp65*** and rpoB,
 for ***identification*** of cultured ***mycobacteria***)

IT Gene, microbial
 RL: ANT (Analyte); ANST (Analytical study)

(***hsp65*** ; comparative evaluation of polymerase chain reaction and restriction enzyme analysis using two amplified targets, ***hsp65*** and rpoB, for ***identification*** of cultured ***mycobacteria***)

IT Human (infection; comparative evaluation of polymerase chain reaction and restriction enzyme analysis using two amplified targets, ***hsp65*** and rpoB, for ***identification*** of cultured ***mycobacteria***)

IT ***Diagnosis*** (mol.; comparative evaluation of polymerase chain reaction and restriction enzyme analysis using two amplified targets, ***hsp65*** and rpoB, for ***identification*** of cultured ***mycobacteria***)

IT PCR (polymerase chain reaction) (restriction enzyme anal. (PCR-REA); comparative evaluation of polymerase chain reaction and restriction enzyme anal. using two amplified targets, ***hsp65*** and rpoB, for ***identification*** of cultured ***mycobacteria***)

IT Gene, microbial
 RL: ANT (Analyte); ANST (Analytical study)
 (rpoB; comparative evaluation of polymerase chain reaction and restriction enzyme analysis using two amplified targets, ***hsp65*** and rpoB, for ***identification*** of cultured ***mycobacteria***)

L9 ANSWER 35 OF 71 CAPLUS COPYRIGHT 2009 ACS on STN
 AN 2005:171452 CAPLUS <LOGINID:20090617>>
 DN 143:279938

TI Multicenter evaluation of ***mycobacteria*** ***identification*** by PCR restriction enzyme analysis in laboratories from Latin America and the Caribbean

AU Leao, Sylvia Cardoso; Bernardelli, Amelia; Cataldi, Angel; Zumarraga, Martin; Robledo, Jaime; Realpe, Teresa; Mejia, Gloria Isabel; Da Silva Telles, Maria Alice; Chimara, Erica; Velazco, Maritza; Fernandez, Jorge; Rodrigues, Pamela Araya; Guerrero, Martha Inirida; Leon, Clara Ines; Porras, Tania Bibiana; Rastogi, Nalin; Goh, Khye Seng; Suffys, Philip; Da Silva Rocha, Adalgisa; Dos Santos Netto, Diogo; Ritacco, Viviana; Lopez, Beatriz; Barrera, Lucia; Palomino, Juan Carlos; Martin, Anandi; Portaeels, Françoise

CS Departamento de Microbiologia, Imunologia e Parasitologia, Universidade Federal de Sao Paulo-Escola Paulista de Medicina, Sao Paulo, 04023-062, Brazil

SO Journal of Microbiological Methods (2005), 61(2), 193-199
 CODEN: JMIHQ; ISSN: 0167-7012

PB Elsevier B.V.
 DT Journal
 LA English
 AB The ***identification*** of ***mycobacterial*** species in clin. isolates is essential for making patient care decisions. Polymerase chain reaction (PCR) restriction enzyme anal. (PRA) is a simple and rapid ***identification*** method, based on amplification of 441 bp of the ***hsp65*** gene and restriction with BstEII and HaeIII. As a contribution to the validation of PRA, a multicenter study was performed in eight labs. located in Argentina, Brazil, Colombia, Chile, and Guadeloupe. Each lab. received 18 coded isolates from the collection of the Institute of Tropical Medicine (Antwerp, Belgium), representing

duplicates of nine lab. strains: ***Mycobacterium*** terrae CIPT 140320001, ***Mycobacterium*** scrofulaceum CIPT 140220031, ***Mycobacterium*** flavesens ATCC 14474, ***Mycobacterium*** triviale ATCC 23292, ***Mycobacterium*** nonchromogenicum ATCC 19530, ***Mycobacterium*** chitae ATCC 19627, ***Mycobacterium*** abscessus ATCC 19977, ***Mycobacterium*** kansasii ATCC 12478, and ***Mycobacterium*** peregrinum ATCC 14467. A detailed protocol including amplification, enzymic digestion, and gel prepn. was provided to each lab. Two labs. ***identified*** correctly all 18 (100%) isolates, one ***identified*** correctly 17 (94.5%), two ***identified*** 14 (77.7%), one ***identified*** 11 (61%), and two ***identified*** 8 (44.4%) isolates. Errors detected in labs. with

more than 77% accuracy were assocd. with electrophoresis running conditions and an unspecific amplicon produced by a single strain. Lower accuracy was mainly related to inappropriate use of DNA markers and insufficient training in interpretation of patterns. In conclusion, the PRA method was readily implemented in some Latin American and Caribbean labs. of ***mycobacteria***, but improvements in crit. points, as gel running conditions and training in interpretation of patterns, are needed in order to improve accuracy. In others, improvement in crit. points is still necessary.

RE.CNT 17 THERE ARE 17 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

TI Multicenter evaluation of ***mycobacteria*** ***identification*** by PCR restriction enzyme analysis in laboratories from Latin America and the Caribbean

AB The ***identification*** of ***mycobacterial*** species in clin. isolates is essential for making patient care decisions. Polymerase chain reaction (PCR) restriction enzyme anal. (PRA) is a simple and rapid ***identification*** method, based on amplification of 441 bp of the ***hsp65*** gene and restriction with BstEII and HaeIII. As a contribution to the validation of PRA, a multicenter study was performed. . . 18 coded isolates from the collection of the Institute of Tropical Medicine (Antwerp, Belgium), representing duplicates of nine lab. strains: ***Mycobacterium*** terrae CIPT 140320001, ***Mycobacterium*** scrofulaceum CIPT 140220031, ***Mycobacterium*** flavesens ATCC 14474, ***Mycobacterium*** triviale ATCC 23292, ***Mycobacterium*** nonchromogenicum ATCC 19530, ***Mycobacterium*** chitae ATCC 19627, ***Mycobacterium*** abscessus ATCC 19977, ***Mycobacterium*** kansasii ATCC 12478, and ***Mycobacterium*** peregrinum ATCC 14467. A detailed protocol including amplification, enzymic digestion, and gel prepn. was provided to each lab. Two labs. ***identified*** correctly all 18 (100%) isolates, one ***identified*** correctly 17 (94.5%), two ***identified*** 14 (77.7%), one ***identified*** 11 (61%), and two ***identified*** 8 (44.4%) isolates. Errors detected in labs. with

more than 77% accuracy were assocd. with electrophoresis running conditions and an. . . in interpretation of patterns. In conclusion, the PRA method was readily implemented in some Latin American and Caribbean labs. of ***mycobacteria***, but improvements in crit. points, as gel running conditions and training in interpretation of patterns, are needed in order to. . .

ST ***Mycobacterium*** PCR restriction enzyme analysis
IT Gene, microbial
RL: ANT (Analyte); ANST (Analytical study)

(***hsp65*** ; multicenter evaluation of ***mycobacteria***
 identification by PCR restriction enzyme anal. in labs. from
 Latin America and Caribbean)

IT ***Mycobacterium***
 Mycobacterium abscessus
 Mycobacterium chitae
 Mycobacterium flavescens
 Mycobacterium kansasii
 Mycobacterium nonchromogenicum
 Mycobacterium peregrinum
 Mycobacterium scrofulaceum
 Mycobacterium terrae
 Mycobacterium triviale
 PCR (polymerase chain reaction)
 (multicenter evaluation of ***mycobacteria***
 identification by PCR restriction enzyme anal. in labs. from
 Latin America and Caribbean)

IT 81295-18-3 93229-61-9, Restriction endonuclease, BstEII
 RL: ARG (Analytical reagent use); BUU (Biological use, unclassified); ANST
 (Analytical study); BIOL (Biological study); USES (Uses)
 (multicenter evaluation of ***mycobacteria***
 identification by PCR restriction enzyme anal. in labs. from
 Latin America and Caribbean)

IT 864193-17-9 864193-18-0
 RL: ARG (Analytical reagent use); BUU (Biological use, unclassified); DGN
 (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL
 (Biological study); USES (Uses)
 (***primer*** ; multicenter evaluation of ***mycobacteria***
 identification by PCR restriction enzyme anal. in labs. from
 Latin America and Caribbean)

L9 ANSWER 36 OF 71 CAPLUS COPYRIGHT 2009 ACS on STN
 AN 2005:81792 CAPLUS <<LOGINID:20090617>>
 DN 143:20521

TI Rapid species ***identification*** within the ***Mycobacterium***
 chelonae-abscessus group by high-resolution melting analysis of
 hsp65 PCR products

AU Odell, Ian D.; Cloud, Joann L.; Seipp, Michael; Wittwer, Carl T.
 CS Department of Pathology, University of Utah Medical School, Salt Lake
 City, USA
 SO American Journal of Clinical Pathology (2005), 123(1), 96-101
 CODEN: AJCPAI; ISSN: 0002-9173
 PB American Society of Clinical Pathology
 DT Journal
 LA English
 AB Polymerase chain reaction (PCR) amplification of the heat shock protein 65
 (***hsp65***) gene followed by high-resoln. melting anal. with LCGreen
 I (Idaho Technol., Salt Lake City, UT) was used to differentiate the
 mycobacteria species ***Mycobacterium*** chelonae,
 Mycobacterium abscessus, and ***Mycobacterium*** immunogenum
 in less than 20 min. A 105-base-pair amplicon that clustered the
 different species by predicted melting temp. was found from available
 GenBank ***hsp65*** sequences. We ***identified*** 24 clin.
 isolates within the M chelonae-abscessus group by proximal 16S rRNA and
 hsp65 gene sequencing. Rapid-cycle PCR followed by high-resoln.
 melting anal. clustered these samples into the following groups: M
 abscessus, 12; M abscessus sequence variant, 2; M chelonae, 7; unexpected

M chelonae sequence variant, 1; and M immunogenum, 2. The M chelonae variant had a single base change not found in reported GenBank sequences. Advantages of the method include speed, low risk of amplicon contamination (closed-tube), and no need for sepn. steps (sequencing, electrophoresis, high-performance liq. chromatog.) or real-time monitoring.

RE.CNT 23 THERE ARE 23 CITED REFERENCES AVAILABLE FOR THIS RECORD

ALL CITATIONS AVAILABLE IN THE RE FORMAT

TI Rapid species ***identification*** within the ***Mycobacterium*** chelonae-abscessus group by high-resolution melting analysis of ***hsp65*** PCR products

AB Polymerase chain reaction (PCR) amplification of the heat shock protein 65 (***hsp65***) gene followed by high-resoln. melting anal. with LCGreen I (Idaho Technol., Salt Lake City, UT) was used to differentiate the ***Mycobacterium*** species ***Mycobacterium*** chelonae, ***Mycobacterium*** abscessus, and ***Mycobacterium*** immunogenum in less than 20 min. A 105-base-pair amplicon that clustered the different species by predicted melting temp. was found from available GenBank ***hsp65*** sequences. We ***identified*** 24 clin. isolates within the M chelonae-abscessus group by proximal 16S rRNA and ***hsp65*** gene sequencing. Rapid-cycle PCR followed by high-resoln. melting anal. clustered these samples into the following groups: M abscessus, 12; M. . .

ST PCR melting analysis ***Mycobacterium*** gene ***hsp65***

IT Heat-shock proteins
RL: BSU (Biological study, unclassified); BIOL (Biological study) (HSP 65; species ***identification*** within ***Mycobacterium*** chelonae-abscessus group by high-resoln. melting anal. of ***hsp65*** PCR products)

IT Gene, microbial
RL: ANT (Analyte); DGN (Diagnostic use); ANST (Analytical study); BIOL (Biological study); USES (Uses) (***hsp65*** ; species ***identification*** within ***Mycobacterium*** chelonae-abscessus group by high-resoln. melting anal. of ***hsp65*** PCR products)

IT Nucleic acid hybridization (melting anal.; species ***identification*** within ***Mycobacterium*** chelonae-abscessus group by high-resoln. melting anal. of ***hsp65*** PCR products)

IT ***Diagnosis*** (mol.; species ***identification*** within ***Mycobacterium*** chelonae-abscessus group by high-resoln. melting anal. of ***hsp65*** PCR products)

IT Human
Mycobacterium abscessus
Mycobacterium chelonae
Mycobacterium immunogenum
PCR (polymerase chain reaction) (species ***identification*** within ***Mycobacterium*** chelonae-abscessus group by high-resoln. melting anal. of ***hsp65*** PCR products)

IT ***Primers*** (nucleic acid)
RL: ARG (Analytical reagent use); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses) (species ***identification*** within ***Mycobacterium*** chelonae-abscessus group by high-resoln. melting anal. of ***hsp65*** PCR products)

IT Genotyping (method)

(species ***identification*** ; species ***identification***
within ***Mycobacterium*** chelonae-abscessus group by high-resoln.
melting anal. of ***hsp65*** PCR products)
IT 853031-88-6 853031-89-7
RL: ARG (Analytical reagent use); DGN (Diagnostic use); PRP (Properties);
ANST (Analytical study); BIOL (Biological study); USES (Uses)
(PCR ***primer*** ; species ***identification*** within
Mycobacterium chelonae-abscessus group by high-resoln. melting
anal. of ***hsp65*** PCR products)

L9 ANSWER 37 OF 71 CAPLUS COPYRIGHT 2009 ACS ON STN

AN 2005:69709 CAPLUS <<LOGINID:20090617>>

DN 143:1806

TI A new method for species ***identification*** and differentiation of
Mycobacterium chelonae complex based on amplified ***hsp65***
restriction analysis (AHSPPRA)

AU Selvaraju, Suresh B.; Khan, Izhar U. H.; Yadav, Jagjit S.

CS Molecular Toxicology Division, Department of Environmental Health,
University of Cincinnati Medical Center, Cincinnati, OH, 45267-0056, USA

SO Molecular and Cellular Probes (2005), 19(2), 93-99

CODEN: MCPRE6; ISSN: 0890-8508

PB Elsevier B.V.

DT Journal

LA English

AB Members of the ***Mycobacterium*** chelonae complex (MCC), namely M.
chelonae, ***Mycobacterium*** abscessus and ***Mycobacterium***
immunogenum, have been implicated in nosocomial infections and
occupational respiratory illnesses like hypersensitivity pneumonitis (HP)
assocd. with contaminated metalworking fluid (MWF) exposures. Close
relationship among these member species makes their differentiation
cumbersome using the existing methods. Here we report a simple and rapid
method for unambiguous ***identification*** and differentiation of the
three-member species of the MCC group with PCR-restriction anal. targeting
a 667-bp segment of a variable region of the 65-kDa-heat shock protein (
hsp65) gene. This assay, described as Amplified ***hsp65***
Restriction Anal. (AHSPPRA), can discriminate all the three individual
species using a one-step restriction digestion using either BbvI or
Eco1091. The enzyme NarI can differentiate M. immunogenum from the other
two MCC species (M. chelonae and M. abscessus). The developed method was
validated using several non-MCC ref. species of other rapidly growing
mycobacteria (RGM) and MCC field isolates from MWF samples.
Direct cell-lysis was used instead of the conventional DNA template
prepn., which improved the rapidity, simplicity and adaptability of the
developed method. The results suggest that the developed method can
unambiguously differentiate species of the M. chelonae complex from other
RGM species and from one another.

RE.CNT 20 THERE ARE 20 CITED REFERENCES AVAILABLE FOR THIS RECORD

ALL CITATIONS AVAILABLE IN THE RE FORMAT

TI A new method for species ***identification*** and differentiation of
Mycobacterium chelonae complex based on amplified ***hsp65***
restriction analysis (AHSPPRA)

AB Members of the ***Mycobacterium*** chelonae complex (MCC), namely M.
chelonae, ***Mycobacterium*** abscessus and ***Mycobacterium***
immunogenum, have been implicated in nosocomial infections and
occupational respiratory illnesses like hypersensitivity pneumonitis (HP)
assocd. with contaminated metalworking fluid. . . member species makes
their differentiation cumbersome using the existing methods. Here we

report a simple and rapid method for unambiguous ***identification*** and differentiation of the three-member species of the MCC group with PCR-restriction anal. targeting a 667-bp segment of a variable region of the 65-kDa-heat shock protein (***hsp65***) gene. This assay, described as Amplified ***hsp65*** Restriction Anal. (AHSRA), can discriminate all the three individual species using a one-step restriction digestion using either BbvI or Eco01091. . . species (M. chelonae and M. abscessus). The developed method was validated using several non-MCC ref. species of other rapidly growing ***mycobacteria*** (RGM) and MCC field isolates from MWF samples. Direct cell-lysis was used instead of the conventional DNA template prepn., which. . .

ST sequence ***Mycobacterium*** gene ***hsp65*** PCR
diagnosis

IT Heat-shock proteins
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(HSP 65; PCR method for species ***identification*** and differentiation of ***Mycobacterium*** chelonae complex based on gene ***hsp65***)

IT DNA sequences
Mycobacterium abscessus
Mycobacterium chelonae
Mycobacterium immunogenum
PCR (polymerase chain reaction)
Protein sequences
RFLP (restriction fragment length polymorphism)
Respiratory system, disease
(PCR method for species ***identification*** and differentiation of ***Mycobacterium*** chelonae complex based on gene ***hsp65***)

IT ***Primers*** (nucleic acid)
RL: ARG (Analytical reagent use); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(PCR method for species ***identification*** and differentiation of ***Mycobacterium*** chelonae complex based on gene ***hsp65***)

IT Human
(***diagnosis*** in; PCR method for species ***identification*** and differentiation of ***Mycobacterium*** chelonae complex based on gene ***hsp65***)

IT Gene, microbial
RL: ANT (Analyte); BSU (Biological study, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(***hsp65*** ; PCR method for species ***identification*** and differentiation of ***Mycobacterium*** chelonae complex based on gene ***hsp65***)

IT ***Diagnosis***
(mol.; PCR method for species ***identification*** and differentiation of ***Mycobacterium*** chelonae complex based on gene ***hsp65***)

IT 852345-32-5 852345-33-6
RL: ARG (Analytical reagent use); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(PCR ***primer*** ; PCR method for species ***identification*** and differentiation of ***Mycobacterium*** chelonae complex based on gene ***hsp65***)

IT 824883-12-7 824883-14-9 824883-16-1
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL

(Biological study)
 (amino acid sequence; PCR method for species ***identification***
 and differentiation of ***Mycobacterium*** chelonae complex based
 on gene ***hsp65***)

IT 824883-11-6 824883-13-8 824883-15-0
 RI: ANT (Analyte); BSU (Biological study, unclassified); DGN (Diagnostic
 use); PRP (Properties); ANST (Analytical study); BIOL (Biological study);
 USES (Uses)
 (nucleotide sequence; PCR method for species ***identification***
 and differentiation of ***Mycobacterium*** chelonae complex based
 on gene ***hsp65***)

L9 ANSWER 38 OF 71 CAPLUS COPYRIGHT 2009 ACS on STN
 AN 2004:973914 CAPLUS <<LOGINID::20090617>>
 DN 142:170995

TI Method for simultaneous detection of Tubercle bacillus (TB) and
 nontuberculous ***mycobacteria*** (NTM) by multiple-nested polymerase
 chain reaction
 IN Kim, Eun Ha; Park, Yeong Seok
 PA Biocore Co., Ltd., S. Korea
 SO Repub. Korean Kongkai Taeho Kongbo, No pp. given
 CODEN: KRXXA7
 DT Patent
 LA Korean
 FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	KR 2003075315		20030926	KR 2002-14466	20020318
PRAI	KR 2002-14466	A	20020318		

AB A method for simultaneous detection of tubercle Bacillus (TB) and
 nontuberculous ***Mycobacteria*** (NTM) by multiple-nested polymerase
 chain reaction is provided, thereby rapidly detecting tubercle Bacillus
 and nontuberculous ***Mycobacteria***. A method for simultaneous
 detection of tubercle Bacillus (TB) and nontuberculous
 Mycobacteria (NTM) comprises carrying out multiple-nested
 polymerase chain reaction using all of three kinds of ***primer***
 pairs specific to mtp40, IS6110 and ***hsp65***, resp., which are
 assocd. with ***Mycobacteria***, wherein the ***primer*** pairs
 have the nucleotide sequences of SEQ ID NOs: 1 to 12. The method for
 simultaneous detection of tubercle Bacillus (TB) and nontuberculous
 Mycobacteria (NTM) comprises the steps of: adding DNA extd. from
 infected microorganism and three kinds of ***primers*** of SEQ ID NOs:
 1 to 12 into a patient's sample; amplifying a portion or the total of the
 gene by multiple-nested polymerase chain reaction; and analyzing the
 amplified products.

TI Method for simultaneous detection of Tubercle bacillus (TB) and
 nontuberculous ***mycobacteria*** (NTM) by multiple-nested polymerase
 chain reaction

AB A method for simultaneous detection of tubercle Bacillus (TB) and
 nontuberculous ***Mycobacteria*** (NTM) by multiple-nested polymerase
 chain reaction is provided, thereby rapidly detecting tubercle Bacillus
 and nontuberculous ***Mycobacteria***. A method for simultaneous
 detection of tubercle Bacillus (TB) and nontuberculous
 Mycobacteria (NTM) comprises carrying out multiple-nested
 polymerase chain reaction using all of three kinds of ***primer***
 pairs specific to mtp40, IS6110 and ***hsp65***, resp., which are
 assocd. with ***Mycobacteria***, wherein the ***primer*** pairs

have the nucleotide sequences of SEQ ID NOs: 1 to 12. The method for simultaneous detection of tubercle Bacillus (TB) and nontuberculous ***Mycobacteria*** (NTM) comprises the steps of: adding DNA extd. from infected microorganism and three kinds of ***primers*** of SEQ ID NOs: 1 to 12 into a patient's sample; amplifying a portion or the total of the gene. . .

ST Tubercle bacillus nontuberculous ***mycobacteria*** ***diagnosis***
 primer PCR

IT Gene, microbial
 RL: BSU (Biological study, unclassified); DGN (Diagnostic use); BIOL (Biological study); USES (Uses)
 (IS6110; method for simultaneous detection of Tubercle bacillus (TB) and nontuberculous ***mycobacteria*** (NTM) by multiple-nested polymerase chain reaction)

IT Gene, microbial
 RL: BSU (Biological study, unclassified); DGN (Diagnostic use); BIOL (Biological study); USES (Uses)
 (***hsp65*** ; method for simultaneous detection of Tubercle bacillus (TB) and nontuberculous ***mycobacteria*** (NTM) by multiple-nested polymerase chain reaction)

IT ***Diagnosis***
 Mycobacterium tuberculosis
 (method for simultaneous detection of Tubercle bacillus (TB) and nontuberculous ***mycobacteria*** (NTM) by multiple-nested polymerase chain reaction)

IT ***Primers*** (nucleic acid)
 RL: ARG (Analytical reagent use); DGN (Diagnostic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
 (method for simultaneous detection of Tubercle bacillus (TB) and nontuberculous ***mycobacteria*** (NTM) by multiple-nested polymerase chain reaction)

IT Gene, microbial
 RL: BSU (Biological study, unclassified); DGN (Diagnostic use); BIOL (Biological study); USES (Uses)
 (mtp40; method for simultaneous detection of Tubercle bacillus (TB) and nontuberculous ***mycobacteria*** (NTM) by multiple-nested polymerase chain reaction)

IT PCR (polymerase chain reaction)
 (nested; method for simultaneous detection of Tubercle bacillus (TB) and nontuberculous ***mycobacteria*** (NTM) by multiple-nested polymerase chain reaction)

IT ***Mycobacterium***
 (nontuberculous; method for simultaneous detection of Tubercle bacillus (TB) and nontuberculous ***mycobacteria*** (NTM) by multiple-nested polymerase chain reaction)

IT DNA sequences
 (of ***primers*** ; method for simultaneous detection of Tubercle bacillus (TB) and nontuberculous ***mycobacteria*** (NTM) by multiple-nested polymerase chain reaction)

L9 ANSWER 39 OF 71 CAPLUS COPYRIGHT 2009 ACS on STN
 AN 2004:727349 CAPLUS <<LOGINID::20090617>>
 DN 142:87110
 TI Capillary electrophoretic restriction fragment length polymorphism patterns for the ***mycobacterial*** ***hsp65*** gene
 AU Ho, Hsin-Tsung; Chang, Po-Ling; Hung, Chia-Chien; Chang, Huan-Tsung
 CS Department of Laboratory Medicine, Mackay Memorial Hospital, Taipei,

Taiwan
SO Journal of Clinical Microbiology (2004), 42(8), 3525-3531
CODEN: JCMIDW; ISSN: 0095-1137
PB American Society for Microbiology
DT Journal
LA English
AB PCR-restriction fragment length polymorphism (RFLP) anal. is a nonprobe method for the rapid ***identification*** of ***Mycobacterium*** species. We demonstrate the sepn. of DNA or restriction fragments digested from the ***mycobacterial*** gene encoding the 65-kDa heat shock protein (***hsp65***) by capillary electrophoresis (CE). By using a pair of unlabeled ***primers***, Tbl1 and Tbl2, and only one restriction enzyme, HaeIII, we investigated a total of 52 ref. and clin. strains encompassing 12 ***Mycobacterium*** species. The electrophoretic sepn. of high-resoln. CE required <20 min and was capable of ***identifying*** fragments as small as 12 bp. A good agreement of measurement was obsd. between the sizes of restriction fragments resolved by CE, and the real sizes were deduced from the sequence anal. Distinct differentiations were also well demonstrated between some species and subspecies by an extra HaeIII digestion site. With the advantage of the complete RFLP pattern available from CE, it appears to be more convenient to use an electropherogram rather than performing the cumbersome slab gel electrophoresis plus ***diagnostic*** algorithm to ***identify*** ***Mycobacterium*** species. Beyond the agarose and polyacrylamide gel electrophoresis, high-resoln. CE provides an alternative for rapid ***identification*** of ***Mycobacterium*** species that is feasible for automation and routine use without the need for costly probes.

RE.CNT 17 THERE ARE 17 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

TI Capillary electrophoretic restriction fragment length polymorphism patterns for the ***mycobacterial*** ***hsp65*** gene

AB PCR-restriction fragment length polymorphism (RFLP) anal. is a nonprobe method for the rapid ***identification*** of ***Mycobacterium*** species. We demonstrate the sepn. of DNA or restriction fragments digested from the ***mycobacterial*** gene encoding the 65-kDa heat shock protein (***hsp65***) by capillary electrophoresis (CE). By using a pair of unlabeled ***primers***, Tbl1 and Tbl2, and only one restriction enzyme, HaeIII, we investigated a total of 52 ref. and clin. strains encompassing 12 ***Mycobacterium*** species. The electrophoretic sepn. of high-resoln. CE required <20 min and was capable of ***identifying*** fragments as small as 12 bp. A good agreement of measurement was obsd. between the sizes of restriction fragments resolved. . . CE, it appears to be more convenient to use an electropherogram rather than performing the cumbersome slab gel electrophoresis plus ***diagnostic*** algorithm to ***identify*** ***Mycobacterium*** species. Beyond the agarose and polyacrylamide gel electrophoresis, high-resoln. CE provides an alternative for rapid ***identification*** of ***Mycobacterium*** species that is feasible for automation and routine use without the need for costly probes.

ST RFLP capillary electrophoresis genotyping ***Mycobacterial*** ***hsp65*** gene

IT Heat-shock proteins

RL: BSU (Biological study, unclassified); BIOL (Biological study) (HSP 65, gene for; capillary electrophoretic restriction fragment length polymorphism patterns for ***mycobacterial*** ***hsp65*** gene)

IT PCR (polymerase chain reaction)
 RFLP (restriction fragment length polymorphism)
 (PCR-RFLP; capillary electrophoretic restriction fragment length
 polymorphism patterns for ***mycobacterial*** ***hsp65*** gene)

IT Capillary electrophoresis
 Genotyping (method)
 Mycobacterium
 Mycobacterium abscessus
 Mycobacterium asiaticum
 Mycobacterium avium
 Mycobacterium chelonae chelonae
 Mycobacterium fortuitum
 Mycobacterium gastris
 Mycobacterium gordonae
 Mycobacterium intracellulare
 Mycobacterium kansasii
 Mycobacterium phlei
 Mycobacterium smegmatis
 Mycobacterium tuberculosis
 (capillary electrophoretic restriction fragment length polymorphism
 patterns for ***mycobacterial*** ***hsp65*** gene)

IT Gene, microbial
 RL: ANT (Analyte); BSU (Biological study, unclassified); ANST (Analytical
 study); BIOL (Biological study)
 (for heat shock protein ***hsp65*** ; capillary electrophoretic
 restriction fragment length polymorphism patterns for
 mycobacterial ***hsp65*** gene)

IT Human
 (human infection; capillary electrophoretic restriction fragment length
 polymorphism patterns for ***mycobacterial*** ***hsp65*** gene)

IT 81295-18-3
 RL: ARG (Analytical reagent use); ANST (Analytical study); USES (Uses)
 (capillary electrophoretic restriction fragment length polymorphism
 patterns for ***mycobacterial*** ***hsp65*** gene)

L9 ANSWER 40 OF 71 CAPLUS COPYRIGHT 2009 ACS on STN
 AN 2004:715776 CAPLUS <<LOGINID:20090617>>
 DN 142:255259
 TI LightCycler-based differentiation of ***Mycobacterium*** abscessus and
 Mycobacterium chelonae
 AU Sedlacek, L.; Rifai, M.; Feldmann, K.; Bange, F. C.
 CS Department of Medical Microbiology and Hospital Epidemiology, Medical
 School Hannover, Hannover, 30625, Germany
 SO Journal of Clinical Microbiology (2004), 42(7), 3284-3287
 CODEN: JCMIDW; ISSN: 0095-1137
 PB American Society for Microbiology
 DT Journal
 LA English
 AB In this study we introduce a rapid procedure to ***identify***
 Mycobacterium abscessus (types I and II) and M. chelonae using
 LightCycler-based anal. of the ***hsp65*** gene. Results from 36
 clin. strains were compared with ***hsp65*** gene restriction anal.
 and biochem. profiles of bacilli. As all three methods yielded identical
 results for each isolate, this procedure offers an excellent alternative
 to previously established nucleic acid amplification-based techniques for
 the ***diagnosis*** of ***mycobacterial*** diseases.

RE.CNT 14 THERE ARE 14 CITED REFERENCES AVAILABLE FOR THIS RECORD

ALL CITATIONS AVAILABLE IN THE RE FORMAT

- TI LightCycler-based differentiation of ***Mycobacterium*** abscessus and
Mycobacterium chelonae
- AB In this study we introduce a rapid procedure to ***identify***
Mycobacterium abscessus (types I and II) and M. chelonae using
LightCycler-based anal. of the ***hsp65*** gene. Results from 36
clin. strains were compared with ***hsp65*** gene restriction anal.
and biochem. profiles of bacilli. As all three methods yielded identical
results for each isolate, this procedure offers an excellent alternative
to previously established nucleic acid amplification-based techniques for
the ***diagnosis*** of ***mycobacterial*** diseases.
- ST ***Mycobacterium*** differentiation LightCycler PCR ***primer***
probe sequence; ***hsp65*** 16S rRNA gene detection PCR
Mycobacterium
- IT Gene, microbial
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(16 S rRNA; LightCycler-based differentiation of ***Mycobacterium***
abscessus and ***Mycobacterium*** chelonae)
- IT rRNA
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(16 S, gene; LightCycler-based differentiation of ***Mycobacterium***
abscessus and ***Mycobacterium*** chelonae)
- IT ***Mycobacterium*** abscessus
Mycobacterium chelonae
(LightCycler-based differentiation of ***Mycobacterium*** abscessus
and ***Mycobacterium*** chelonae)
- IT ***Primers*** (nucleic acid)
RL: ARG (Analytical reagent use); BUU (Biological use, unclassified); DGN
(Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL
(Biological study); USES (Uses)
(LightCycler-based differentiation of ***Mycobacterium*** abscessus
and ***Mycobacterium*** chelonae)
- IT DNA sequences
(PCR ***primers*** ; LightCycler-based differentiation of
Mycobacterium abscessus and ***Mycobacterium*** chelonae)
- IT RFLP (restriction fragment length polymorphism)
(RFLP-PCR; LightCycler-based differentiation of ***Mycobacterium***
abscessus and ***Mycobacterium*** chelonae)
- IT Gene, microbial
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(***hsp65*** ; LightCycler-based differentiation of
Mycobacterium abscessus and ***Mycobacterium*** chelonae)
- IT ***Diagnosis***
(mol.; LightCycler-based differentiation of ***Mycobacterium***
abscessus and ***Mycobacterium*** chelonae)
- IT PCR (polymerase chain reaction)
(multiplex, LightCycler; LightCycler-based differentiation of
Mycobacterium abscessus and ***Mycobacterium*** chelonae)
- IT 245670-26-2D, LC Red 640, conjugates with hybridization probes
RL: ARG (Analytical reagent use); BUU (Biological use, unclassified); DGN
(Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL
(Biological study); USES (Uses)
(LC Red 640; LightCycler-based differentiation of ***Mycobacterium***
abscessus and ***Mycobacterium*** chelonae)
- IT 251949-03-8D, LC-RED 705, conjugates with hybridization probes
RL: ARG (Analytical reagent use); BUU (Biological use, unclassified); DGN
(Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL

(Biological study); USES (Uses)
 (LC Red 705; LightCycler-based differentiation of ***Mycobacterium***
 abscessus and ***Mycobacterium*** chelonae)

II 2321-07-5D, Fluorescein, conjugates with hybridization probes
 RL: ARG (Analytical reagent use); BUU (Biological use, unclassified); DGN
 (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL
 (Biological study); USES (Uses)
 (LightCycler-based differentiation of ***Mycobacterium*** abscessus
 and ***Mycobacterium*** chelonae)

II 845683-14-9
 RL: ARG (Analytical reagent use); BUU (Biological use, unclassified); DGN
 (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL
 (Biological study); USES (Uses)
 (***primer*** sequence, Tb_11; LightCycler-based differentiation of
 Mycobacterium abscessus and ***Mycobacterium*** chelonae)

II 845683-15-0
 RL: ARG (Analytical reagent use); BUU (Biological use, unclassified); DGN
 (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL
 (Biological study); USES (Uses)
 (***primer*** sequence, Tb_12; LightCycler-based differentiation of
 Mycobacterium abscessus and ***Mycobacterium*** chelonae)

II 845683-18-3D, 3'-conjugate with fluorescein
 RL: ARG (Analytical reagent use); BUU (Biological use, unclassified); DGN
 (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL
 (Biological study); USES (Uses)
 (probe sequence, LC_68; LightCycler-based differentiation of
 Mycobacterium abscessus and ***Mycobacterium*** chelonae)

II 845683-19-4D, 5'-conjugate with LightCycler Red 705
 RL: ARG (Analytical reagent use); BUU (Biological use, unclassified); DGN
 (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL
 (Biological study); USES (Uses)
 (probe sequence, LC_86; LightCycler-based differentiation of
 Mycobacterium abscessus and ***Mycobacterium*** chelonae)

II 845683-16-1D, 3'-conjugate with fluorescein
 RL: ARG (Analytical reagent use); BUU (Biological use, unclassified); DGN
 (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL
 (Biological study); USES (Uses)
 (probe sequence, LC_98; LightCycler-based differentiation of
 Mycobacterium abscessus and ***Mycobacterium*** chelonae)

II 845683-17-2D, 5'-conjugate with LightCycler Red 640
 RL: ARG (Analytical reagent use); BUU (Biological use, unclassified); DGN
 (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL
 (Biological study); USES (Uses)
 (probe sequence, LC_99; LightCycler-based differentiation of
 Mycobacterium abscessus and ***Mycobacterium*** chelonae)

II 7647-14-5, Sodium chloride, biological studies
 RL: BSU (Biological study, unclassified); BIOL (Biological study)
 (tolerance, of ***Mycobacterium*** ; LightCycler-based
 differentiation of ***Mycobacterium*** abscessus and
 Mycobacterium chelonae)

II 994-36-5, Sodium citrate
 RL: BSU (Biological study, unclassified); BIOL (Biological study)
 (utilization, by ***Mycobacterium*** ; LightCycler-based
 differentiation of ***Mycobacterium*** abscessus and
 Mycobacterium chelonae)

AN 2004:642461 CAPLUS <<LOGINID::20090617>>
DN 141:406390
TI Standardization of in-house polymerase chain reaction for the
identification of ***Mycobacterium*** tuberculosis at the
Reference Tropical Disease Hospital in the State of Goias, Brazil
AU Rodrigues, Marcia Alves Vasconcelos; Serafini, Alvaro Bisol; Pereira,
Marieta de Souza; Dias da Silva, Thathiane; Rabahi, Marcelo Fouad; Lemes
de Alves, Suelly; Kipnis, Andre
CS Departamento de Microbiologia, Instituto de Patologia Tropical e Saude
Publica, Universidade Federal de Goias, Goiania, 74605-050, Brazil
SO Memorias do Instituto Oswaldo Cruz (2004), 99(4), 415-419
CODEN: MIOCAS; ISSN: 0074-0276
PB Instituto Oswaldo Cruz
DT Journal
LA English
AB This study compares smear, growth in Lowenstein-Jensen medium, and inhouse
polymerase chain reaction (PCR) techniques for the detection of
Mycobacterium tuberculosis. A total of 72 specimens from 72
patients with clin. symptoms of tuberculosis, including 70 sputum and two
bronchial aspirate samples, were tested in parallel by smear, culture, and
inhouse PCR techniques. From these, 48 (66.6%) were neg. by the 3
methods, 2 (2.8%) were smear pos. and neg. by culture and inhouse PCR, 11
(15.3%) were both smear and culture neg., and inhouse PCR pos., 7 (9.7%)
were pos. by the 3 methods, 2 (2.8%) were pos. by smear and culture, and
neg. by PCR, 2 (2.8%) were pos. by culture and PCR, but smear neg. After
the resolu. of discrepancies in PCR results, the sensitivity and
specificity for inhouse PCR technique to M. tuberculosis relative to the
culture, were 81.8% and 81.9%, resp. These results confirm that this
method, inhouse PCR, may be a sensitive and specific technique for M.
tuberculosis detection, occurring in both pos. and neg. smear and neg.
cultures.

RE.CNT 36 THERE ARE 36 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

TI Standardization of in-house polymerase chain reaction for the
identification of ***Mycobacterium*** tuberculosis at the
Reference Tropical Disease Hospital in the State of Goias, Brazil
AB This study compares smear, growth in Lowenstein-Jensen medium, and inhouse
polymerase chain reaction (PCR) techniques for the detection of
Mycobacterium tuberculosis. A total of 72 specimens from 72
patients with clin. symptoms of tuberculosis, including 70 sputum and two
bronchial. . .

ST PCR ***Mycobacterium*** tuberculosis ***diagnosis*** gene
hsp65

IT ***Mycobacterium*** tuberculosis
Tuberculosis
(PCR ***diagnosis*** for ***Mycobacterium*** tuberculosis)
IT ***Primers*** (nucleic acid)
RL: ARG (Analytical reagent use); DGN (Diagnostic use); PRP (Properties);
ANST (Analytical study); BIOL (Biological study); USES (Uses)
(PCR ***diagnosis*** for ***Mycobacterium*** tuberculosis)

IT Sputum
(anal. matrix; PCR ***diagnosis*** for ***Mycobacterium***
tuberculosis)

IT Bronchi
(aspirates, anal. matrix; PCR ***diagnosis*** for
Mycobacterium tuberculosis)

IT Human

(***diagnosis*** in; PCR ***diagnosis*** for
 Mycobacterium tuberculosis)

IT Gene, microbial
 RL: ANT (Analyte); ANST (Analytical study)
 (***hsp65*** ; PCR ***diagnosis*** for ***Mycobacterium***
 tuberculosis)

IT ***Diagnosis***
 (mol.; PCR ***diagnosis*** for ***Mycobacterium***
 tuberculosis)

IT PCR (polymerase chain reaction)
 (nested; PCR ***diagnosis*** for ***Mycobacterium***
 tuberculosis)

IT 792989-28-7 792989-29-8 792989-30-1 792989-31-2
 RL: ARG (Analytical reagent use); DGN (Diagnostic use); PRP (Properties);
 ANST (Analytical study); BIOL (Biological study); USES (Uses)
 (PCR ***primer*** for ***Mycobacterium*** gene ***hsp65*** ;
 PCR ***diagnosis*** for ***Mycobacterium*** tuberculosis)

L9 ANSWER 42 OF 71 CAPLUS COPYRIGHT 2009 ACS ON STN

AN 2004:287934 CAPLUS <<LOGINID:20090617>>

DN 140:282411

TI Molecular size markers and methods for ***identification*** of
 Mycobacteria species by PCR and restriction enzyme analysis

IN Koeksalan, Orhan Kaya; Kocagoez, Tanil

PA Turk.

SO PCT Int. Appl., 12 pp.

CODEN: PIXXD2

DT Patent

LA English

FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 2004029296	A2	20040408	WO 2003-TR82	20030926
	WO 2004029296	A3	20040902		
	W:	AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW			
	RW:	GH, GM, KE, LS, MN, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, RO, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG			
	AU 2003276821	A1	20040419	AU 2003-276821	20030926
	TR 200501010	T2	20050523	TR 2005-1010	20030926
	US 20060121479	A1	20060608	US 2005-528453	20051011
PRAI	TR 2002-2252	A	20020926		
	WO 2003-TR82	W	20030926		

AB This invention consists of DNA mol. size markers which are used to det. in a correct and easy way the size of DNA fragments in the evaluation step of the sizes of DNA restriction fragments sepd. by electrophoresis, of the
 hsp65 PCR-REA method used for species ***identification*** of
 mycobacteria .

RE.CNT 2 THERE ARE 2 CITED REFERENCES AVAILABLE FOR THIS RECORD

ALL CITATIONS AVAILABLE IN THE RE FORMAT

TI Molecular size markers and methods for ***identification*** of

Mycobacteria species by PCR and restriction enzyme analysis
 AB . . . size of DNA fragments in the evaluation step of the sizes of DNA
 restriction fragments sepd. by electrophoresis, of the ***hsp65***
 PCR-REA method used for species ***identification*** of
 mycobacterias .
 ST ***Mycobacterium*** species ***identification*** PCR restriction
 enzyme analysis marker
 IT Gene, microbial
 RL: ANT (Analyte); DGN (Diagnostic use); ANST (Analytical study); BIOL
 (Biological study); USES (Uses)
 (***hsp65*** , amplification of; mol. size markers and methods for
 identification of ***Mycobacteria*** species by PCR and
 restriction enzyme anal.)
 IT Gel electrophoresis
 Molecular cloning
 Mycobacterium
 Mycobacterium chitae
 Mycobacterium gallinarum
 Mycobacterium intracellulare
 Mycobacterium simiae
 Mycobacterium smegmatis
 Mycobacterium terrae
 Mycobacterium tuberculosis
 Mycobacterium xenopi
 Nucleic acid amplification (method)
 PCR (polymerase chain reaction)
 Species differences
 (mol. size markers and methods for ***identification*** of
 Mycobacteria species by PCR and restriction enzyme anal.)
 IT ***Primers*** (nucleic acid)
 RL: ARG (Analytical reagent use); DGN (Diagnostic use); PRP (Properties);
 ANST (Analytical study); BIOL (Biological study); USES (Uses)
 (mol. size markers and methods for ***identification*** of
 Mycobacteria species by PCR and restriction enzyme anal.)
 IT ***Diagnosis***
 (mol.; mol. size markers and methods for ***identification*** of
 Mycobacteria species by PCR and restriction enzyme anal.)
 IT 675887-28-2 675887-29-3
 RL: ARG (Analytical reagent use); DGN (Diagnostic use); PRP (Properties);
 ANST (Analytical study); BIOL (Biological study); USES (Uses)
 (TB11 ***primer*** sequence; mol. size markers and methods for
 identification of ***Mycobacteria*** species by PCR and
 restriction enzyme anal.)
 IT 9075-08-5, Restriction enzyme 81295-18-3 93229-61-9, Restriction
 endonuclease, BstEII
 RL: ARG (Analytical reagent use); DGN (Diagnostic use); ANST (Analytical
 study); BIOL (Biological study); USES (Uses)
 (mol. size markers and methods for ***identification*** of
 Mycobacteria species by PCR and restriction enzyme anal.)
 L9 ANSWER 43 OF 71 CAPLUS COPYRIGHT 2009 ACS on STN
 AN 2004;121485 CAPLUS <<LOGINID:20090617>>
 DN 140:298231
 IT Development of a single-tube, cell lysis-based, genus-specific PCR method
 for rapid ***identification*** of ***mycobacteria*** : optimization
 of cell lysis, PCR ***primers*** and conditions, and restriction
 pattern analysis

AU Khan, Izhar U. H.; Yadav, Jagjit S.
 CS Molecular Toxicology Division, Department of Environmental Health,
 University of Cincinnati Medical Center, Cincinnati, OH, 45267-0056, USA
 SO Journal of Clinical Microbiology (2004), 42(1), 453-457
 CODEN: JCMIDW; ISSN: 0095-1137
 PB American Society for Microbiology
 DT Journal
 LA English
 AB A single-tube PCR method was developed for efficient
 identification of nontuberculous ***mycobacteria*** (NTM) and
 their environmental isolates in about 3 h without conventional DNA
 isolation. The following three steps were optimized or developed: (i) a
 simple, 6-min direct cell lysis protocol as a PCR prestep for generation
 of DNA-template; (ii) an improved ***Mycobacterium*** -specific PCR
 amplification protocol with a broader species specificity using newly
 designed ***primers*** targeting a 228-bp region of the 65-kDa heat
 shock protein (hsp) gene and optimal PCR amplification conditions; and
 (iii) a genus-specific restriction anal. of the PCR product for conclusive
 identification of the unknown NTM isolates.
 RE.CNT 22 THERE ARE 22 CITED REFERENCES AVAILABLE FOR THIS RECORD
 ALL CITATIONS AVAILABLE IN THE RE FORMAT
 TI Development of a single-tube, cell lysis-based, genus-specific PCR method
 for rapid ***identification*** of ***mycobacteria*** : optimization
 of cell lysis, PCR ***primers*** and conditions, and restriction
 pattern analysis
 AB A single-tube PCR method was developed for efficient
 identification of nontuberculous ***mycobacteria*** (NTM) and
 their environmental isolates in about 3 h without conventional DNA
 isolation. The following three steps were optimized or. . . developed:
 (i) a simple, 6-min direct cell lysis protocol as a PCR prestep for
 generation of DNA-template; (ii) an improved ***Mycobacterium***
 -specific PCR amplification protocol with a broader species specificity
 using newly designed ***primers*** targeting a 228-bp region of the
 65-kDa heat shock protein (hsp) gene and optimal PCR amplification
 conditions; and (iii) a genus-specific restriction anal. of the PCR
 product for conclusive ***identification*** of the unknown NTM
 isolates.
 ST DNA sequence gene hsp ***Mycobacterium*** isolate MJY3; protein
 HSP65 sequence ***Mycobacterium*** isolate MJY3; gene hsp
 specific PCR restriction analysis ***identification*** nontuberculous
 mycobacteria
 IT ***Primers*** (nucleic acid)
 RL: ARG (Analytical reagent use); BUU (Biological use, unclassified); DGN
 (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL
 (Biological study); USES (Uses)
 (DNA; use of gene hsp genus-specific PCR method followed by restriction
 anal. in rapid ***identification*** of nontuberculous
 mycobacteria)
 IT Heat-shock proteins
 RL: BSU (Biological study, unclassified); PRP (Properties); BIOL
 (Biological study)
 (HSP 65; partial amino acid sequence of 65-kDa heat shock protein from
 Mycobacterium strain M-JY3)
 IT PCR (polymerase chain reaction)
 (development and optimization of single-tube cell lysis-based gene hsp
 genus-specific PCR method for rapid ***identification*** of
 nontuberculous ***mycobacteria***)

IT Gene, microbial
 RL: ANT (Analyte); BUU (Biological use, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
 (hsp; development and optimization of single-tube cell lysis-based gene hsp genus-specific PCR method for rapid ***identification*** of nontuberculous ***mycobacteria***)

IT DNA sequences
 (partial DNA sequence of 65-kDa heat shock protein gene hsp amplified from ***Mycobacterium*** strain M-JY3 using developed genus-specific PCR)

IT Protein sequences
 (partial amino acid sequence of 65-kDa heat shock protein from ***Mycobacterium*** strain M-JY3)

IT DNA
 RL: ARG (Analytical reagent use); BUU (Biological use, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
 (***primer*** ; use of gene hsp genus-specific PCR method followed by restriction anal. in rapid ***identification*** of nontuberculous ***mycobacteria***)

IT ***Mycobacterium***
 (use of gene hsp genus-specific PCR method followed by restriction anal. in rapid ***identification*** of nontuberculous ***mycobacteria***)

IT 638110-92-6
 RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
 (amino acid sequence; partial amino acid sequence of 65-kDa heat shock protein from ***Mycobacterium*** strain M-JY3)

IT 676577-44-9 676577-45-0 676577-46-1 676577-47-2
 RL: ARG (Analytical reagent use); BUU (Biological use, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
 (gene hsp-specific ***primer*** ; use of gene hsp genus-specific PCR method followed by restriction anal. in rapid ***identification*** of nontuberculous ***mycobacteria***)

IT 638110-91-5
 RL: ANT (Analyte); BUU (Biological use, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
 (nucleotide sequence; partial DNA sequence of 65-kDa heat shock protein gene hsp amplified from ***Mycobacterium*** strain M-JY3 using developed genus-specific PCR)

L9 ANSWER 44 OF 71 CAPLUS COPYRIGHT 2009 ACS on STN
 AN 2003:591378 CAPLUS <<LOGINID::20090617>>
 DN 139:146183
 TI ***Primers*** for amplifying ***mycobacterial*** heat shock protein HSP 65 gene and use for ***identifying*** ***mycobacterial*** species
 IN Kim, Bum-joon; Kook, Yoon-ho; Kim, Jeong-mi
 PA Biomedlab Corporation, S. Korea
 SO PCT Int. Appl., 102 pp.
 CODEN: PIXXD2
 DT Patent
 LA English

FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 2003062470	A1	20030731	WO 2003-KR131	20030121
	W:	AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW			
	RW:	GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG			
	KR 2003063935	A	20030731	KR 2002-4297	20020124
	KR 2003072087	A	20030913	KR 2002-11648	20020305
	US 20050014157	A1	20050120	US 2004-500586	20040909
PRAI	KR 2002-4297	A	20020124		
	KR 2002-11648	A	20020305		
	WO 2003-KR131	W	20030121		

AB The present invention relates to a pair of ***primers*** specific to ***mycobacterial*** species, a polynucleotide of an HSP 65 gene fragment, and a method for the ***identification*** of ***mycobacterial*** species by using the same. More specifically, the 604-bp HSP 65 gene fragment can be applied to ***identification*** methods of ***mycobacteria*** such as the comparative sequence anal. method, the probe hybridization method, and PCR-RFLP, which can resolve the problems of a conventional ***identification*** method based on biochem. characteristics, where the genus ***mycobacterium*** covers various species and has a low growth rate, and of the problems of 16S rDNA. Thus, according to the ***identification*** method of the present invention, the ***mycobacterial*** species can be ***identified*** simply, economically, and accurately.

RE.CNT 5 THERE ARE 5 CITED REFERENCES AVAILABLE FOR THIS RECORD

ALL CITATIONS AVAILABLE IN THE RE FORMAT

TI ***Primers*** for amplifying ***mycobacterial*** heat shock protein HSP 65 gene and use for ***identifying*** ***mycobacterial*** species

AB The present invention relates to a pair of ***primers*** specific to ***mycobacterial*** species, a polynucleotide of an HSP 65 gene fragment, and a method for the ***identification*** of ***mycobacterial*** species by using the same. More specifically, the 604-bp HSP 65 gene fragment can be applied to ***identification*** methods of ***mycobacteria*** such as the comparative sequence anal. method, the probe hybridization method, and PCR-RFLP, which can resolve the problems of a conventional ***identification*** method based on biochem. characteristics, where the genus ***mycobacterium*** covers various species and has a low growth rate, and of the problems of 16S rDNA. Thus, according to the ***identification*** method of the present invention, the ***mycobacterial*** species can be ***identified*** simply, economically, and accurately.

ST ***primer*** ***mycobacteria*** heat shock protein ***hsp65*** gene

IT Nucleic acid amplification (method) (DNA; ***primers*** for amplifying ***mycobacterial*** heat shock protein HSP 65 gene and use for ***identifying*** ***mycobacterial*** species)

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IT  Heat-shock proteins
    RL: ARG (Analytical reagent use); BPN (Biosynthetic preparation); BSU
        (Biological study, unclassified); DGN (Diagnostic use); PRP (Properties);
        ANST (Analytical study); BIOL (Biological study); PREP (Preparation); USES
        (Uses)
        (HSP 65; ***primers*** for amplifying ***mycobacterial*** heat
          shock protein HSP 65 gene and use for ***identifying***
            ***mycobacterial*** species)

IT  Gene, microbial
    RL: ARG (Analytical reagent use); BSU (Biological study, unclassified);
        DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL
        (Biological study); USES (Uses)
        (HSP 65; ***primers*** for amplifying ***mycobacterial*** heat
          shock protein HSP 65 gene and use for ***identifying***
            ***mycobacterial*** species)

IT  ***Diagnosis***
    (mol.; ***primers*** for amplifying ***mycobacterial*** heat
      shock protein HSP 65 gene and use for ***identifying***
        ***mycobacterial*** species)

IT  DNA sequences
    ***Mycobacterium***
    ***Mycobacterium*** BCG
    ***Mycobacterium*** abscessus
    ***Mycobacterium*** africanum
    ***Mycobacterium*** aichiense
    ***Mycobacterium*** asiaticum
    ***Mycobacterium*** avium
    ***Mycobacterium*** avium paratuberculosis
    ***Mycobacterium*** bovis
    ***Mycobacterium*** celatum
    ***Mycobacterium*** chelonae
    ***Mycobacterium*** chitae
    ***Mycobacterium*** farcinogenes
    ***Mycobacterium*** flavescens
    ***Mycobacterium*** fortuitum
    ***Mycobacterium*** gastri
    ***Mycobacterium*** genavense
    ***Mycobacterium*** gordonae
    ***Mycobacterium*** haemophilum
    ***Mycobacterium*** interjectum
    ***Mycobacterium*** intracellulare
    ***Mycobacterium*** kansasii
    ***Mycobacterium*** leprae
    ***Mycobacterium*** malmoense
    ***Mycobacterium*** marinum
    ***Mycobacterium*** microti
    ***Mycobacterium*** mucogenicum
    ***Mycobacterium*** neoaurum
    ***Mycobacterium*** nonchromogenicum
    ***Mycobacterium*** parafortuitum
    ***Mycobacterium*** peregrinum
    ***Mycobacterium*** phlei
    ***Mycobacterium*** scrofulaceum
    ***Mycobacterium*** senegalense
    ***Mycobacterium*** shimoidei
    ***Mycobacterium*** simiae
    ***Mycobacterium*** smegmatis

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Mycobacterium szulgai
 Mycobacterium terrae
 Mycobacterium thermoresistibile
 Mycobacterium triviale
 Mycobacterium tuberculosis
 Mycobacterium ulcerans
 Mycobacterium vaccae
 Mycobacterium wolinskyi
 Nocardia carnea
 RFLP (restriction fragment length polymorphism)
 Tsukamurella paurometabola
 Tsukamurella pulmonis
 Tsukamurella tyrosinosolvens
 (***primers*** for amplifying ***mycobacterial*** heat shock
 protein HSP 65 gene and use for ***identifying***
 mycobacterial species)
 IT ***Primers*** (nucleic acid)
 RL: ARG (Analytical reagent use); BPN (Biosynthetic preparation); BSU
 (Biological study, unclassified); DGN (Diagnostic use); PRP (Properties);
 ANST (Analytical study); BIOL (Biological study); PREP (Preparation); USES
 (Uses)
 (***primers*** for amplifying ***mycobacterial*** heat shock
 protein HSP 65 gene and use for ***identifying***
 mycobacterial species)
 IT 569430-56-4 569432-08-2 569432-09-3 569432-10-6 569432-11-7
 569432-12-8 569432-13-9 569432-14-0 569432-15-1 569432-16-2
 569432-17-3 569432-18-4 569432-19-5 569432-20-8 569432-21-9
 569432-22-0 569432-23-1 569432-24-2 569432-25-3 569432-26-4
 569432-27-5 569432-28-6 569432-29-7 569432-30-0 569432-31-1
 569432-32-2 569432-33-3 569432-34-4 569432-35-5 569432-36-6
 569432-37-7 569432-38-8 569432-39-9 569432-40-2 569432-41-3
 569432-42-4 569432-43-5 569432-44-6 569432-45-7 569432-46-8
 569432-47-9 569432-48-0 569432-49-1 569432-50-4 569432-51-5
 569432-52-6 569432-53-7 569432-54-8 569432-55-9
 RL: ARG (Analytical reagent use); BSU (Biological study, unclassified);
 DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL
 (Biological study); USES (Uses)
 (nucleotide sequence; ***primers*** for amplifying
 mycobacterial heat shock protein HSP 65 gene and use for
 identifying ***mycobacterial*** species)
 IT 569432-56-0
 RL: ARG (Analytical reagent use); BSU (Biological study, unclassified);
 DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL
 (Biological study); USES (Uses)
 (***primer*** HSPF3 sequence; ***primers*** for amplifying
 mycobacterial heat shock protein HSP 65 gene and use for
 identifying ***mycobacterial*** species)
 IT 569432-57-1
 RL: ARG (Analytical reagent use); BSU (Biological study, unclassified);
 DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL
 (Biological study); USES (Uses)
 (***primer*** HSPR3 sequence; ***primers*** for amplifying
 mycobacterial heat shock protein HSP 65 gene and use for
 identifying ***mycobacterial*** species)
 IT 81295-43-4, Nuclease, restriction endodeoxyribo-, Xho I
 RL: BUU (Biological use, unclassified); BIOL (Biological study); USES
 (Uses)

(***primers*** for amplifying ***mycobacterial*** heat shock protein HSP 65 gene and use for ***identifying***
 mycobacterial species)

II 569477-29-8
 RL: PRP (Properties)
 (unclaimed sequence; ***primers*** for amplifying
 mycobacterial heat shock protein HSP 65 gene and use for
 identifying ***mycobacterial*** species)

L9 ANSWER 45 OF 71 CAPLUS COPYRIGHT 2009 ACS on STN
 AN 2002:88707 CAPLUS <LOGINID::20090617>>
 DN 137:227047

TI Application of molecular biology techniques to the ***diagnosis*** of
 nontuberculous ***mycobacterial*** infections

AU Ruiz, M.; Rodriguez, J. C.; Escribano, I.; Garcia-Martinez, J.;
 Rodriguez-Valera, F.; Royo, G.

CS S. Microbiologia, Hospital General Universitario de Elche, Alicante,
 03203, Spain

SO APMIS (2001), 109(12), 857-864
 CODEN: APMSEL; ISSN: 0903-4641

PB Munksgaard International Publishers Ltd.
 DT Journal
 LA English

AB A total of 19,723 clin. samples were cultivated for the detection of
 mycobacteria from Jan. 1995 to Mar. 2001. The 203 strains of
 nontuberculous ***mycobacteria*** isolated were ***identified***
 with the use of mol. techniques in combination with traditional biochem.
 tests. The mol. methods applied were PCR-restriction fragment length
 polymorphism anal. (PRA) alone, or in combination with 16S rRNA and
 16S-23S spacer sequencing. The patient records of those with specimens
 pos. for ***mycobacteria*** were analyzed to evaluate the clin.
 significance of the culture results. Twenty-five of the 124 patients
 analyzed (20%) were regarded as having clin. ***mycobacteriosis***.
 The main species assoc. with ***mycobacteriosis*** were:
 Mycobacterium avium (13 cases), M. intracellulare (2 cases), M.
 kansasii (5 cases), M. chelonae (2 cases), M. malmoense (1 case), M.
 scrofulaceum (1 case) and M. marinum (1 case). The use of PRA alone or in
 combination with gene sequencing provided valuable help in discerning
 mycobacteria at both the intra- and interspecies level, thus
 contributing to a faster and more efficient ***diagnosis*** and
 epidemiol. follow-up.

RE.CNT 47 THERE ARE 47 CITED REFERENCES AVAILABLE FOR THIS RECORD
 ALL CITATIONS AVAILABLE IN THE RE FORMAT

TI Application of molecular biology techniques to the ***diagnosis*** of
 nontuberculous ***mycobacterial*** infections

AB A total of 19,723 clin. samples were cultivated for the detection of
 mycobacteria from Jan. 1995 to Mar. 2001. The 203 strains of
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 with the use of mol. techniques in combination with traditional biochem.
 tests. The mol. methods applied were PCR-restriction fragment length.
 . alone, or in combination with 16S rRNA and 16S-23S spacer sequencing.
 The patient records of those with specimens pos. for ***mycobacteria***
 were analyzed to evaluate the clin. significance of the culture results.
 Twenty-five of the 124 patients analyzed (20%) were regarded as having
 clin. ***mycobacteriosis***. The main species assoc. with
 mycobacteriosis were: ***Mycobacterium*** avium (13 cases),

intracellulare (2 cases), *M. kansasii* (5 cases), *M. chelonae* (2 cases), *M. mageritense* (1 case), *M. . . . M. marinum* (1 case). The use of PRA alone or in combination with gene sequencing provided valuable help in discerning ***mycobacteria*** at both the intra- and interspecies level, thus contributing to a faster and more efficient ***diagnosis*** and epidemiol. follow-up.

ST PCR RFLP 16S rDNA ITS sequence nontuberculous ***Mycobacterium***
detection; DNA sequence ***Mycobacterium*** 16S 23S rDNA ITS;
primer ***diagnosis*** nontuberculous ***mycobacterial***
infection PCR RFLP; human Spain HIV ***Mycobacterium*** infection
detection method PRA

IT rRNA
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(16 S; DNA sequence of complete 16S rRNA gene, ITS region, and partial
sequence of 23S rRNA gene found in ***Mycobacterium*** avium)

IT rRNA
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(23 S; DNA sequence of complete 16S rRNA gene, ITS region, and partial
sequence of 23S rRNA gene found in ***Mycobacterium*** avium)

IT DNA sequences
Mycobacterium avium
(DNA sequence of complete 16S rRNA gene, ITS region, and partial
sequence of 23S rRNA gene found in ***Mycobacterium*** avium)

IT ***Primers*** (nucleic acid)
RL: ARG (Analytical reagent use); DGN (Diagnostic use); PRP (Properties);
ANST (Analytical study); BIOL (Biological study); USES (Uses)
(DNA; use of PCR-RFLP alone or in combination with 16S rDNA and ITS
sequencing for detection of nontuberculous ***Mycobacterium***
species in various clin. samples obtained from patients also infected
with HIV)

IT Genetic element
RL: ANT (Analyte); BSU (Biological study, unclassified); DGN (Diagnostic
use); PRP (Properties); ANST (Analytical study); BIOL (Biological study);
USES (Uses)
(ITS (internal transcribed spacer); use of PCR-RFLP alone or in
combination with 16S rDNA and ITS sequencing for detection of
nontuberculous ***Mycobacterium*** species in various clin.
samples)

IT Human groups
(Spanish; use of PCR-RFLP alone or in combination with 16S rDNA and ITS
sequencing for detection of nontuberculous ***Mycobacterium***
species in various clin. samples obtained in Spain)

IT Infection
(bacterial, ***mycobacteriosis*** ; use of PCR-RFLP alone or in
combination with 16S rDNA and ITS sequencing for ***diagnosis*** of
nontuberculous ***mycobacterial*** infections)

IT Gene, microbial
RL: ANT (Analyte); BSU (Biological study, unclassified); DGN (Diagnostic
use); PRP (Properties); ANST (Analytical study); BIOL (Biological study);
USES (Uses)
(for 16S rRNA; use of PCR-RFLP alone or in combination with 16S rDNA
and ITS sequencing for detection of nontuberculous
Mycobacterium species in various clin. samples)

IT Gene, microbial
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL
(Biological study)
(for 23S RNA; DNA sequence of complete 16S rRNA gene, ITS region, and

partial sequence of 23S rRNA gene found in ***Mycobacterium***
avium)

IT Gene, microbial
RL: ANT (Analyte); DGN (Diagnostic use); ANST (Analytical study); BIOL
(Biological study); USES (Uses)
(***hsp65*** ; use of PCR-RFLP alone or in combination with 16S rDNA
and ITS sequencing for detection of nontuberculous
Mycobacterium species in various clin. samples obtained from
patients also infected with HIV)

IT ***Diagnosis***
(mol.; use of PCR-RFLP alone or in combination with 16S rDNA and ITS
sequencing for ***diagnosis*** of nontuberculous
mycobacterial infections)

IT Epidemiology
(mol.; use of PCR-RFLP alone or in combination with 16S rDNA and ITS
sequencing for ***diagnosis*** of nontuberculous
mycobacterial infections, potential use in epidemiol.)

IT DNA
RL: ARG (Analytical reagent use); DGN (Diagnostic use); PRP (Properties);
ANST (Analytical study); BIOL (Biological study); USES (Uses)
(***primer*** ; use of PCR-RFLP alone or in combination with 16S
rDNA and ITS sequencing for detection of nontuberculous
Mycobacterium species in various clin. samples obtained from
patients also infected with HIV)

IT Bone marrow
Feces
PCR (polymerase chain reaction)
RFLP (restriction fragment length polymorphism)
(use of PCR-RFLP alone or in combination with 16S rDNA and ITS
sequencing for detection of nontuberculous ***Mycobacterium***
species in various clin. samples (such as bone marrow, and feces)
obtained from patients also infected with HIV)

IT Blood analysis
Respiratory system
Urine analysis
(use of PCR-RFLP alone or in combination with 16S rDNA and ITS
sequencing for detection of nontuberculous ***Mycobacterium***
species in various clin. samples (such as respiratory tract, urine,
blood) obtained from patients also infected with HIV)

IT Pleural fluid
Skin
(use of PCR-RFLP alone or in combination with 16S rDNA and ITS
sequencing for detection of nontuberculous ***Mycobacterium***
species in various clin. samples (such pleural fluid and skin) obtained
from patients also infected with HIV)

IT Human immunodeficiency virus
(use of PCR-RFLP alone or in combination with 16S rDNA and ITS
sequencing for detection of nontuberculous ***Mycobacterium***
species in various clin. samples obtained from patients also infected
with HIV)

IT Human
Mycobacterium chelonae
Mycobacterium intracellulare
Mycobacterium kansasii
Mycobacterium malmoense
Mycobacterium marinum
Mycobacterium scrofulaceum

(use of PCR-RFLP alone or in combination with 16S rDNA and ITS sequencing for detection of nontuberculous ***Mycobacterium*** species in various clin. samples obtained in Spain)

II 457965-27-4 457965-28-5 458571-15-8
 RL: ARG (Analytical reagent use); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
 (PCR ***primer*** ; use of PCR-RFLP (PRA) alone or in combination with 16S rDNA and ITS sequencing for detection of nontuberculous ***Mycobacterium*** species in various clin. samples obtained from patients also infected with HIV)

II 431974-46-8, GenBank AF410479
 RL: ANT (Analyte); BSU (Biological study, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
 (nucleotide sequence; DNA sequence of complete 16S rRNA gene, ITS region, and partial sequence of 23S rRNA gene found in ***Mycobacterium*** avium)

L9 ANSWER 46 OF 71 CAPLUS COPYRIGHT 2009 ACS ON STN
 AN 2001:647495 CAPLUS <<LOGINID:20090617>>
 DN 136:304792

TI ***Identification*** of 54 ***mycobacterial*** species by PCR-restriction fragment length polymorphism analysis of the ***hsp65*** gene

AU Brunello, Francesca; Ligozzi, Marco; Cristelli, Emanuela; Bonora, Stefano; Tortoli, Enrico; Fontana, Roberta

CS Dipartimento di Patologia, Sezione di Microbiologia, Università di Verona and Servizio di Microbiologia dell'Azienda Ospedaliera di Verona, Verona, 37100, Italy

SO Journal of Clinical Microbiology (2001), 39(8), 2799-2806
 CODEN: JCMIDW; ISSN: 0095-1137

PB American Society for Microbiology
 DT Journal
 LA English

AB A total of 121 ref. and clin. strains of both slowly and rapidly growing ***mycobacteria*** belonging to 54 species were studied for restriction fragment length polymorphism of a PCR-amplified 439-bp segment of the gene encoding the 65-kDa heat shock protein. Restriction digests were sepd. by 10% polyacrylamide gel electrophoresis (PAGE). By including a size std. in each sample, the restriction fragment profile was calcd. using a computer-aided comparison program. An algorithm describing these 54 species (including 22 species not previously described) is proposed. We found that this assay based on 10% PAGE provided a more precise est. than that based on agarose gel electrophoresis of the real size of restriction fragments as deduced from the sequence anal. and allowed
 identification of ***mycobacteria*** whose PCR-restriction fragment length polymorphism anal. patterns were unequivocally
 identified by fragments shorter than 60 bp.

RE.CNT 31 THERE ARE 31 CITED REFERENCES AVAILABLE FOR THIS RECORD
 ALL CITATIONS AVAILABLE IN THE RE FORMAT

TI ***Identification*** of 54 ***mycobacterial*** species by PCR-restriction fragment length polymorphism analysis of the ***hsp65*** gene

AB A total of 121 ref. and clin. strains of both slowly and rapidly growing ***mycobacteria*** belonging to 54 species were studied for restriction fragment length polymorphism of a PCR-amplified 439-bp segment of the gene encoding. . . based on agarose gel electrophoresis of the real size of

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restriction fragments as deduced from the sequence anal. and allowed
***identification*** of ***mycobacteria*** whose PCR-restriction
fragment length polymorphism anal. patterns were unequivocally
***identified*** by fragments shorter than 60 bp.
ST DNA sequence ***Mycobacterium*** gene ***hsp65*** protein;
genotyping PCR RFLP polyacrylamide gel electrophoresis algorithm
***Mycobacterium*** ***hsp65***
IT ***Primers*** (nucleic acid)
RL: ARG (Analytical reagent use); DGN (Diagnostic use); PRP (Properties);
ANST (Analytical study); BIOL (Biological study); USES (Uses)
(DNA; ***identification*** of 54 ***mycobacterial*** species by
PCR-restriction fragment length polymorphism anal. of the ***hsp65***
gene)
IT Heat-shock proteins
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL
(Biological study)
(HSP 65; ***identification*** of 54 ***mycobacterial*** species
by PCR-restriction fragment length polymorphism anal. of the
***hsp65*** gene)
IT RFLP (restriction fragment length polymorphism)
(PCR-; ***identification*** of 54 ***mycobacterial*** species
by PCR-restriction fragment length polymorphism anal. of the
***hsp65*** gene)
IT Gene, microbial
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL
(Biological study)
(gene ***hsp65***; ***identification*** of 54
***mycobacterial*** species by PCR-restriction fragment length
polymorphism anal. of the ***hsp65*** gene)
IT Algorithm
Gel electrophoresis
Genotyping (method)
***Mycobacterium*** abscessus
***Mycobacterium*** agri
***Mycobacterium*** aichiense
***Mycobacterium*** alvei
***Mycobacterium*** asiaticum
***Mycobacterium*** austroafricanum
***Mycobacterium*** avium
***Mycobacterium*** avium paratuberculosis
***Mycobacterium*** branderi
***Mycobacterium*** brumae
***Mycobacterium*** celatum
***Mycobacterium*** chelonae
***Mycobacterium*** chitae
***Mycobacterium*** confluentis
***Mycobacterium*** duvalii
***Mycobacterium*** fallax
***Mycobacterium*** farcinogenes
***Mycobacterium*** fortuitum
***Mycobacterium*** gadium
***Mycobacterium*** gastris
***Mycobacterium*** genavense
***Mycobacterium*** gilvum
***Mycobacterium*** gordonae
***Mycobacterium*** haemophilum
***Mycobacterium*** hiberniae

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***Mycobacterium*** interjectum
***Mycobacterium*** intracellulare
***Mycobacterium*** kansasii
***Mycobacterium*** malmoense
***Mycobacterium*** marinum
***Mycobacterium*** mucogenicum
***Mycobacterium*** neoaurum
***Mycobacterium*** nonchromogenicum
***Mycobacterium*** obuense
***Mycobacterium*** peregrinum
***Mycobacterium*** phlei
***Mycobacterium*** porcinum
***Mycobacterium*** poriferae
***Mycobacterium*** pulveris
***Mycobacterium*** rhodesiae
***Mycobacterium*** scrofulaceum
***Mycobacterium*** senegalense
***Mycobacterium*** shimoidei
***Mycobacterium*** siernhoferi
***Mycobacterium*** simiae
***Mycobacterium*** smegmatis
***Mycobacterium*** szulgai
PCR (polymerase chain reaction)
( ***identification*** of 54 ***mycobacterial*** species by
  PCR-restriction fragment length polymorphism anal. of the ***hsp65***
  gene)
IT Protein sequences
  (of gene ***hsp65*** heat shock protein isolated from
  ***Mycobacterium*** species)
IT DNA sequences
  (of gene ***hsp65*** isolated from ***Mycobacterium*** species)
IT DNA
  RL: ARG (Analytical reagent use); DGN (Diagnostic use); PRP (Properties);
  ANST (Analytical study); BIOL (Biological study); USES (Uses)
  ( ***primer*** ; ***identification*** of 54 ***mycobacterial***
  species by PCR-restriction fragment length polymorphism anal. of the
  ***hsp65*** gene)
IT 409133-45-5 409133-46-6 409133-47-7 409133-48-8 409133-49-9
  409133-50-2 409133-51-3 409133-52-4 409133-53-5 409133-54-6
  409133-55-7 409133-56-8 409133-57-9 409133-58-0 409133-59-1
  409133-60-4 409133-61-5 409133-62-6 409133-63-7 409133-64-8
  409133-65-9 409133-66-0 409133-67-1 409133-68-2 409133-69-3
  409133-70-6 409133-71-7 409133-72-8 409133-73-9 409133-74-0
  409133-75-1 409133-76-2 409133-77-3 409133-78-4 409133-79-5
  409133-80-8 409133-81-9 409133-82-0 409400-81-3 409400-82-4
  409400-83-5 409400-84-6 409400-85-7 409400-86-8 409400-87-9
  409400-88-0
  RL: BSU (Biological study, unclassified); PRP (Properties); BIOL
  (Biological study)
  (amino acid sequence; ***identification*** of 54
  ***mycobacterial*** species by PCR-restriction fragment length
  polymorphism anal. of the ***hsp65*** gene)
IT 81295-18-3 93229-61-9, Restriction endonuclease BstEII
  RL: ARG (Analytical reagent use); DGN (Diagnostic use); ANST (Analytical
  study); BIOL (Biological study); USES (Uses)
  ( ***identification*** of 54 ***mycobacterial*** species by
  PCR-restriction fragment length polymorphism anal. of the ***hsp65***

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gene)

IT	330543-09-4, GenBank AJ310216	330543-10-7, GenBank AJ310217
	330543-11-8, GenBank AJ310218	330543-12-9, GenBank AJ310219
	330543-13-0, GenBank AJ310221	330543-14-1, GenBank AJ310223
	330543-15-2, GenBank AJ310225	330543-16-3, GenBank AJ310226
	330543-17-4, GenBank AJ310229	330543-18-5, GenBank AJ310230
	330543-19-6, GenBank AJ310231	330543-20-9, GenBank AJ310232
	330543-21-0, GenBank AJ310233	330543-22-1, GenBank AJ310236
	330543-23-2, GenBank AJ310238	330777-51-0, GenBank AJ307630
	330777-52-1, GenBank AJ307631	330777-53-2, GenBank AJ307632
	330777-54-3, GenBank AJ307636	330777-55-4, GenBank AJ307640
	330777-56-5, GenBank AJ307641	330777-57-6, GenBank AJ307643
	330777-58-7, GenBank AJ307644	330777-59-8, GenBank AJ307645
	330777-60-1, GenBank AJ307646	330777-61-2, GenBank AJ307647
	330777-62-3, GenBank AJ307651	330777-63-4, GenBank AJ307652
	330777-64-5, GenBank AJ307654	383716-71-0, GenBank AJ310215
	383716-72-1, GenBank AJ310224	383716-73-2, GenBank AJ310228
	383716-75-4, GenBank AJ310237	383716-76-5, GenBank AJ307637
	383716-77-6, GenBank AJ307649	383716-78-7, GenBank AJ307653
	384598-59-8, GenBank AJ310220	384598-71-4, GenBank AJ310234
	384598-73-6, GenBank AJ310235	384598-75-8, GenBank AJ310239
	384598-89-4, GenBank AJ307634	384598-91-8, GenBank AJ307635
	384598-93-0, GenBank AJ307638	384598-95-2, GenBank AJ307639
	384598-97-4, GenBank AJ307648	384598-99-6, GenBank AJ307650
	385635-00-7, GenBank AJ310227	385635-02-9, GenBank AJ307642
	385652-99-3, GenBank AJ310222	385653-01-0, GenBank AJ307633

RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)

(nucleotide sequence; ***identification*** of 54

mycobacterial species by PCR-restriction fragment length

polymorphism anal. of the ***hsp65*** gene)

L9 ANSWER 47 OF 71 CAPLUS COPYRIGHT 2009 ACS on STN

AN 2000:539667 CAPLUS <LOGNID:20090617>

DN 134:247672

TI A multiplex approach to molecular detection of *Brucella abortus* and/or

Mycobacterium *bovis* infection in cattle

AU Sreevatsan, Srinand; Bookout, Jack B.; Ringpis, Fidel; Perumaalla, Veera S.; Ficht, Thomas A.; Adams, L. Garry; Hagius, Sue D.; Elzer, Philip H.; Bricker, Betsy J.; Kumar, Girish K.; Rajasekhar, M.; Isloor, Srikrishna; Barathur, Raj R.

CS ClinCytte, San Diego, CA, 92121, USA

SO Journal of Clinical Microbiology (2000), 38(7), 2602-2610

CODEN: JCMIDW; ISSN: 0095-1137

PB American Society for Microbiology

DT Journal

LA English

AB A multiplex amplification and detection platform for the ***diagnosis*** of ***Mycobacterium*** *bovis* and *Brucella abortus* infection simultaneously in bovine milk and nasal secretions was developed. This system (designated the bovine pathogen detection assay [BPDA]-PCR) consists of duplex amplification of species-specific targets (a region of the BCSP31K gene of *B. abortus* and a repeat-sequence region in the ***hsp65*** gene of *M. bovis*, resp.). This is followed by a solid-phase probe capture hybridization of amplicons for detection. On the basis of spiking expts. with normal milk, the anal. sensitivity of the assay was

800 CFU equiv./mL of milk for *B. abortus* and as low as 4 CFU equiv. per mL of milk for *M. bovis*. BPDA-PCR was validated with 45 liver samples from lemmings exptl. infected with *B. abortus*. The assay sensitivity, based on culture status as a "gold std.," was 93.9%. In this expt., BPDA-PCR also ***identified*** five culture-neg. liver samples as pos. (41.7%).

Field

studies for the evaluation of BPDA-PCR were performed with samples from dairy animals from geog. distinct regions (India, Mexico, and Argentina). A high prevalence of shedding of *B. abortus* (samples from India) and *M. bovis* (samples from Mexico) was ***identified*** by BPDA-PCR. In samples from India, *B. abortus* shedding was ***identified*** in 86% of milk ring test-pos. animals (n = 15) and 80% of milk ring test-neg. cows (n = 5). In samples from Mexico, *M. bovis* was ***identified*** by PCR in 32.6% of pools (n = 46) of milk that each contained milk from 10 animals and in 56.2% of nasal swabs (n = 121) from cattle from tuberculin test-pos. herds. In contrast, the Argentine cattle (n = 70) had a modest prevalence of *M. bovis* shedding in nasal swabs (2.9%) and milk (1.4%) and of *B. abortus* in milk (11.4%). On the basis of these analyses, we

identify BPDA-PCR as an optimal tool for both screening of herds and testing of individual animals in a disease eradication program. A combination of the duplex assay, screening of milk samples in pools, and the proposed algorithm provides a highly sensitive, cost-effective, and economically viable alternative to serol. testing.

RE.CNT 37 THERE ARE 37 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

TI A multiplex approach to molecular detection of *Brucella abortus* and/or ***Mycobacterium*** *bovis* infection in cattle

AB A multiplex amplification and detection platform for the ***diagnosis*** of ***Mycobacterium*** *bovis* and *Brucella abortus* infection simultaneously in bovine milk and nasal secretions was developed. This system (designated the bovine pathogen. . . duplex amplification of species-specific targets (a region of the BCSP31K gene of *B. abortus* and a repeat-sequence region in the ***hsp65*** gene of *M. bovis*, resp.). This is followed by a solid-phase probe capture hybridization of amplicons for detection. On the. . . *B. abortus*. The assay sensitivity, based on culture status as a "gold std.," was 93.9%. In this expt., BPDA-PCR also ***identified*** five culture-neg. liver samples as pos. (41.7%). Field studies for the evaluation of BPDA-PCR were performed with samples from dairy. . . and Argentina). A high prevalence of shedding of *B. abortus* (samples from India) and *M. bovis* (samples from Mexico) was ***identified*** by BPDA-PCR. In samples from India, *B. abortus* shedding was ***identified*** in 86% of milk ring test-pos. animals (n = 15) and 80% of milk ring test-neg. cows (n = 5). In samples from Mexico, *M. bovis* was ***identified*** by PCR in 32.6% of pools (n = 46) of milk that each contained milk from 10 animals and in. . . nasal swabs (2.9%) and milk (1.4%) and of *B. abortus* in milk (11.4%). On the basis of these analyses, we ***identify*** BPDA-PCR as an optimal tool for both screening of herds and testing of individual animals in a disease eradication program. . .

ST mol ***diagnosis*** BPDA PCR hybridization *Brucella* ***Mycobacterium*** infection cattle; bovine pathogen detection assay PCR hybridization *Brucella* ***Mycobacterium***

IT Probes (nucleic acid)

RL: ARG (Analytical reagent use); PRP (Properties); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(*B. abortus* BCSP31K gene and *M. tuberculosis* gene ***hsp65***
-specific ***primers*** ; multiplex approach (BPDA-PCR followed by

probe capture hybridization) to mol. detection of *Brucella abortus* and/or ****Mycobacterium**** *bovis* in milk samples or nasal swabs)

IT Gene, microbial
 RL: ANT (Analyte); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
 (BCSP31K; multiplex approach (BPDA-PCR followed by probe capture hybridization) to mol. detection of *Brucella abortus* and/or ****Mycobacterium**** *bovis* infection in cattle)

IT ***Primers*** (nucleic acid)
 RL: ARG (Analytical reagent use); PRP (Properties); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
 (DNA, *B. abortus* BCSP31K gene and *M. tuberculosis* gene ***hsp65*** -specific ***primers*** ; multiplex approach (BPDA-PCR followed by probe capture hybridization) to mol. detection of *Brucella abortus* and/or ****Mycobacterium**** *bovis* in milk samples or nasal swabs)

IT PCR (polymerase chain reaction)
 (bovine pathogen detection assay [BPDA]-PCR; multiplex approach (BPDA-PCR followed by probe capture hybridization) to mol. detection of *Brucella abortus* and/or ****Mycobacterium**** *bovis* infection in cattle)

IT Gene, microbial
 RL: ANT (Analyte); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
 (***hsp65*** ; multiplex approach (BPDA-PCR followed by probe capture hybridization) to mol. detection of *Brucella abortus* and/or ****Mycobacterium**** *bovis* infection in cattle)

IT *Brucella*
 (infection with, brucellosis; multiplex approach (BPDA-PCR followed by probe capture hybridization) to mol. detection of *Brucella abortus* and/or ****Mycobacterium**** *bovis* infection in cattle)

IT ***Diagnosis***
 (mol.; multiplex approach (BPDA-PCR followed by probe capture hybridization) used in both screening of herds and individual animals for *Brucella abortus* and/or ****Mycobacterium**** *bovis*)

IT Milk
 (multiplex approach (BPDA-PCR followed by probe capture hybridization) to mol. detection of *Brucella abortus* and/or ****Mycobacterium**** *bovis* in milk samples or nasal swabs)

IT *Brucella melitensis*
 Cattle
 ****Mycobacterium**** *bovis*
 Nucleic acid hybridization
 Tuberculosis
 (multiplex approach (BPDA-PCR followed by probe capture hybridization) to mol. detection of *Brucella abortus* and/or ****Mycobacterium**** *bovis* infection in cattle)

IT DNA
 RL: ARG (Analytical reagent use); PRP (Properties); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
 (***primer*** , *B. abortus* BCSP31K gene and *M. tuberculosis* gene ***hsp65*** -specific ***primers*** ; multiplex approach (BPDA-PCR followed by probe capture hybridization) to mol. detection of *Brucella abortus* and/or ****Mycobacterium**** *bovis* in milk samples or nasal swabs)

IT Nose
 (swab of; multiplex approach (BPDA-PCR followed by probe capture hybridization) to mol. detection of *Brucella abortus* and/or

Mycobacterium bovis in milk samples or nasal swabs)

IT 331290-67-6D, biotinylated 331290-68-7D, biotinylated
 RL: ARG (Analytical reagent use); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
 (B. abortus BCSP31K gene-specific ***primer*** ; multiplex approach (BPDA-PCR followed by probe capture hybridization) to mol. detection of Brucella abortus and/or ***Mycobacterium*** bovis in milk samples or nasal swabs)

IT 331290-69-8
 RL: ARG (Analytical reagent use); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
 (B. abortus BCSP31K gene-specific probe; multiplex approach (BPDA-PCR followed by probe capture hybridization) to mol. detection of Brucella abortus and/or ***Mycobacterium*** bovis in milk samples or nasal swabs)

IT 331290-70-1D, biotinylated 331290-71-2D, biotinylated
 RL: ARG (Analytical reagent use); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
 (gene ***hsp65*** M. tuberculosis complex-specific ***primer*** ; multiplex approach (BPDA-PCR followed by probe capture hybridization) to mol. detection of Brucella abortus and/or ***Mycobacterium*** bovis in milk samples or nasal swabs)

IT 331290-72-3
 RL: ARG (Analytical reagent use); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
 (gene ***hsp65*** M. tuberculosis complex-specific probe; multiplex approach (BPDA-PCR followed by probe capture hybridization) to mol. detection of Brucella abortus and/or ***Mycobacterium*** bovis in milk samples or nasal swabs)

L9 ANSWER 48 OF 71 CAPLUS COPYRIGHT 2009 ACS on STN
 AN 2000:122970 CAPLUS <<LOGINID:20090617>>
 DN 133:115654
 TI Species ***identification*** of ***Mycobacterium*** avium complex isolates by a variety of molecular techniques
 AU Beggs, Marjorie L.; Stevanova, Rossina; Eisenach, Kathleen D.
 CS Department of Pathology, J. L. McClellan Memorial Veterans Hospital, University of Arkansas for Medical Sciences, Little Rock, AR, USA
 SO Journal of Clinical Microbiology (2000), 38(2), 508-512
 CODEN: JCMIDW; ISSN: 0095-1137
 PB American Society for Microbiology
 DT Journal
 LA English
 AB Organisms in the ***Mycobacterium*** avium complex (MAC; M. avium, M. intracellulare, and "nonspecific or X" MAC) are emerging pathogens among individual organisms of which significant genetic variability is displayed. The objective of the present study was to evaluate various mol. methods for the rapid and definitive ***identification*** of MAC species. Isolates were obtained from both human immunodeficiency virus (HIV)-pos. patients and HIV-neg. patients with and without known predisposing conditions. The isolates were initially hybridized with nucleic acid probes complementary to the rRNA of the resp. ***mycobacterial*** species (AccuProbe Culture Confirmation kits for M. avium, M. intracellulare, and MAC species; Gen-Probe). Isolates were also examd. by PCR and in some cases by Southern blot hybridization for the insertion element IS1245. Two other techniques included a PCR assay that amplifies the mig gene, a putative virulence factor for MAC, and

hsp65 gene amplification and sequencing. This study led to the following observations. Eighty-five percent of the isolates from HIV-pos. patients were *M. avium* and 86% of the isolates from HIV-neg. patients were *M. intracellulare*. Fifteen of the *M. avium* isolates did not contain IS1245 and 7% of the *M. intracellulare* isolates were found to carry IS1245. All of the *M. avium* strains were mig pos., and all of the *M. intracellulare* strains were mig neg.

RE.CNT 26 THERE ARE 26 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

TI Species ***identification*** of ***Mycobacterium*** *avium* complex isolates by a variety of molecular techniques

AB Organisms in the ***Mycobacterium*** *avium* complex (MAC; *M. avium*, *M. intracellulare*, and "nonspecific or X" MAC) are emerging pathogens among individual organisms of which. . . variability is displayed. The objective of the present study was to evaluate various mol. methods for the rapid and definitive ***identification*** of MAC species. Isolates were obtained from both human immunodeficiency virus (HIV)-pos. patients and HIV-neg. patients with and without known predisposing conditions. The isolates were initially hybridized with nucleic acid probes complementary to the rRNA of the resp. ***mycobacterial*** species (AccuProbe Culture Confirmation kits for *M. avium*, *M. intracellulare*, and MAC species; Gen-Probe). Isolates were also examd. by PCR. . . IS1245. Two other techniques included a PCR assay that amplifies the mig gene, a putative virulence factor for MAC, and

hsp65 gene amplification and sequencing. This study led to the following observations. Eighty-five percent of the isolates from HIV-pos. patients were. . .

ST ***Mycobacterium*** complex isolate ***identification*** PCR hybridization DNA sequence; HIV patient ***Mycobacterium*** isolate ***identification*** PCR hybridization DNA sequence

IT ***Primers*** (nucleic acid)
Primers (nucleic acid)
RL: ARG (Analytical reagent use); PRP (Properties); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(DNA, gene mig-specific ***primers***; species ***identification*** of ***Mycobacterium*** *avium* complex isolates in HIV-pos. and HIV-neg. patients using PCR, nucleic acid hybridization and DNA sequencing)

IT Insertion sequence
RL: ANT (Analyte); ANST (Analytical study)
(IS1245; species ***identification*** of ***Mycobacterium*** *avium* complex isolates in HIV-pos. and HIV-neg. patients using PCR, nucleic acid hybridization and DNA sequencing)

IT Gene, microbial
RL: ANT (Analyte); ANST (Analytical study)
(for 16S rRNA; species ***identification*** of ***Mycobacterium*** *avium* complex isolates in HIV-pos. and HIV-neg. patients using PCR, nucleic acid hybridization and DNA sequencing)

IT Gene, microbial
RL: ANT (Analyte); PRP (Properties); ANST (Analytical study)
(***hsp65***; species ***identification*** of ***Mycobacterium*** *avium* complex isolates in HIV-pos. and HIV-neg. patients using PCR, nucleic acid hybridization and DNA sequencing)

IT Gene, microbial
RL: ANT (Analyte); ANST (Analytical study)
(mig; species ***identification*** of ***Mycobacterium*** *avium* complex isolates in HIV-pos. and HIV-neg. patients using PCR, nucleic

acid hybridization and DNA sequencing)

IT DNA
DNA
RL: ARG (Analytical reagent use); PRP (Properties); THU (Therapeutic use);
ANST (Analytical study); BIOL (Biological study); USES (Uses)
(***primer*** , gene mig-specific ***primers*** ; species
identification of ***Mycobacterium*** avium complex
isolates in HIV-pos. and HIV-neg. patients using PCR, nucleic acid
hybridization and DNA sequencing)

IT Human immunodeficiency virus
Mycobacterium avium
Mycobacterium intracellulare
Nucleic acid hybridization
PCR (polymerase chain reaction)
(species ***identification*** of ***Mycobacterium*** avium
complex isolates in HIV-pos. and HIV-neg. patients using PCR, nucleic
acid hybridization and DNA sequencing)

IT Probes (nucleic acid)
RL: ARG (Analytical reagent use); THU (Therapeutic use); ANST (Analytical
study); BIOL (Biological study); USES (Uses)
(species ***identification*** of ***Mycobacterium*** avium
complex isolates in HIV-pos. and HIV-neg. patients using PCR, nucleic
acid hybridization and DNA sequencing)

IT 285575-58-8
RL: ARG (Analytical reagent use); THU (Therapeutic use); ANST (Analytical
study); BIOL (Biological study); USES (Uses)
(gene mig-specific lower ***primer*** ; species
identification of ***Mycobacterium*** avium complex
isolates in HIV-pos. and HIV-neg. patients using PCR, nucleic acid
hybridization and DNA sequencing)

IT 285575-57-7
RL: ARG (Analytical reagent use); THU (Therapeutic use); ANST (Analytical
study); BIOL (Biological study); USES (Uses)
(gene mig-specific upper ***primer*** ; species
identification of ***Mycobacterium*** avium complex
isolates in HIV-pos. and HIV-neg. patients using PCR, nucleic acid
hybridization and DNA sequencing)

L9 ANSWER 49 OF 71 CAPLUS COPYRIGHT 2009 ACS on STN
AN 1999:782698 CAPLUS <<LOGINID::20090617>>
DN 132:190212
TI Discrimination of members of the ***Mycobacterium*** avium complex by
polymerase chain reaction
AU Sircilli, Marcelo Palma; Roxo, Eliana; Leao, Sylvia Cardoso
CS Departamento de Microbiologia, Imunologia e Parasitologia, Universidade
Federal de Sao Paulo, Escola Paulista de Medicina, Sao Paulo, CEP
04023-062, Brazil
SO Revista de Microbiologia (1999), 30(2), 144-148
CODEN: RMBGBP; ISSN: 0001-3714
PB Sociedade Brasileira de Microbiologia
DT Journal
LA English
AB ***Mycobacterium*** avium complex (MAC) species cannot be
discriminated by the usual methods of biochem. ***identification*** of
mycobacteria . This study showed that amplification by PCR of DT1
and DT6, two single copy sequences ***identified*** in the genome of
M. avium serotype 2, the insertion sequence IS1245, found to be

consistently present in *M. avium* strains and the heat-shock protein gene
 hsp65 , followed by restriction polymorphism anal., are rapid and
 accurate tests for the differentiation of the species *M. avium*, *M.*
intracellulare, and *M. scrofulaceum*.

RE.CNT 18 THERE ARE 18 CITED REFERENCES AVAILABLE FOR THIS RECORD

ALL CITATIONS AVAILABLE IN THE RE FORMAT

TI Discrimination of members of the ***Mycobacterium*** avium complex by
 polymerase chain reaction

AB ***Mycobacterium*** avium complex (MAC) species cannot be
 discriminated by the usual methods of biochem. ***identification*** of
 mycobacteria . This study showed that amplification by PCR of DT1
 and DT6, two single copy sequences ***identified*** in the genome of
M. avium serotype 2, the insertion sequence IS1245, found to be
 consistently present in *M. avium* strains and the heat-shock protein gene
 hsp65 , followed by restriction polymorphism anal., are rapid and
 accurate tests for the differentiation of the species *M. avium*, *M.*
intracellulare, . . .

ST PCR ***identification*** ***Mycobacterium*** avium complex

IT Gene, microbial
 RL: ANT (Analyte); BUU (Biological use, unclassified); ANST (Analytical
 study); BIOL (Biological study); USES (Uses)
 (DT1; discrimination of members of the ***Mycobacterium*** avium
 complex by polymerase chain reaction)

IT Gene, microbial
 RL: ANT (Analyte); BUU (Biological use, unclassified); ANST (Analytical
 study); BIOL (Biological study); USES (Uses)
 (DT6; discrimination of members of the ***Mycobacterium*** avium
 complex by polymerase chain reaction)

IT Taxonomy
 (Discrimination of members of the ***Mycobacterium*** avium complex
 by polymerase chain reaction)

IT Insertion sequence
 RL: ANT (Analyte); BUU (Biological use, unclassified); ANST (Analytical
 study); BIOL (Biological study); USES (Uses)
 (IS1245; discrimination of members of the ***Mycobacterium*** avium
 complex by polymerase chain reaction)

IT ***Mycobacterium*** scrofulaceum
 PCR (polymerase chain reaction)
 RFLP (restriction fragment length polymorphism)
 (discrimination of members of the ***Mycobacterium*** avium complex
 by polymerase chain reaction)

IT Gene, microbial
 RL: ANT (Analyte); BUU (Biological use, unclassified); ANST (Analytical
 study); BIOL (Biological study); USES (Uses)
 (***hsp65*** ; discrimination of members of the
 Mycobacterium avium complex by polymerase chain reaction)

IT ***Mycobacterium*** avium
 (member of MAC complex; discrimination of members of the
 Mycobacterium avium complex by polymerase chain reaction)

IT ***Mycobacterium*** intracellulare
 (member of the MAC complex; discrimination of members of the
 Mycobacterium avium complex by polymerase chain reaction)

IT 148908-89-8
 RL: ARG (Analytical reagent use); BUU (Biological use, unclassified); ANST
 (Analytical study); BIOL (Biological study); USES (Uses)
 (AV6 PCR ***primer*** to DT6; discrimination of members of the
 Mycobacterium avium complex by polymerase chain reaction)

IT 148908-88-7
 RL: ARG (Analytical reagent use); BUU (Biological use, unclassified); ANST (Analytical study); BIOL (Biological study); USES (Uses)
 (AV7 PCR ***primer*** to DT6; discrimination of members of the ***Mycobacterium*** avium complex by polymerase chain reaction)

IT 260042-37-3
 RL: ARG (Analytical reagent use); BUU (Biological use, unclassified); ANST (Analytical study); BIOL (Biological study); USES (Uses)
 (IN38 PCR ***primer*** to DT1; discrimination of members of the ***Mycobacterium*** avium complex by polymerase chain reaction)

IT 148909-28-8
 RL: ARG (Analytical reagent use); BUU (Biological use, unclassified); ANST (Analytical study); BIOL (Biological study); USES (Uses)
 (IN41 PCR ***primer*** to DT1; discrimination of members of the ***Mycobacterium*** avium complex by polymerase chain reaction)

IT 190977-48-1
 RL: ARG (Analytical reagent use); BUU (Biological use, unclassified); ANST (Analytical study); BIOL (Biological study); USES (Uses)
 (P1 PCR ***primer*** to IS1245; discrimination of members of the ***Mycobacterium*** avium complex by polymerase chain reaction)

IT 260042-38-4
 RL: ARG (Analytical reagent use); BUU (Biological use, unclassified); ANST (Analytical study); BIOL (Biological study); USES (Uses)
 (P2 PCR ***primer*** to IS1245; discrimination of members of the ***Mycobacterium*** avium complex by polymerase chain reaction)

IT 150951-89-6
 RL: ARG (Analytical reagent use); BUU (Biological use, unclassified); ANST (Analytical study); BIOL (Biological study); USES (Uses)
 (Tb11 PCR ***primer*** for PRA; discrimination of members of the ***Mycobacterium*** avium complex by polymerase chain reaction)

IT 150951-90-9
 RL: ARG (Analytical reagent use); BUU (Biological use, unclassified); ANST (Analytical study); BIOL (Biological study); USES (Uses)
 (Tb12 PCR ***primer*** for PRA; discrimination of members of the ***Mycobacterium*** avium complex by polymerase chain reaction)

L9 ANSWER 50 OF 71 CAPLUS COPYRIGHT 2009 ACS ON STN

AN 1999:595536 CAPLUS <<LOGINID:20090617>>

DN 132:118005

TI Determination of the sensitivity and specificity of PCR assays using different target DNAs for the detection of ***Mycobacterium*** tuberculosis

AU Wei, Cheng-Yu; Lee, Chun N.; Chu, Chin-Hwa; Hwang, Jiuan Jiuan; Lee, Chan Ping

CS Tzu Chi College of Medicine and Humanities, Tzu Chi General Hospital, Hualien, Taiwan

SO Kaohsiung Journal of Medical Sciences (1999), 15(7), 396-405
 CODEN: KJMSFM; ISSN: 0257-5655

PB Kaohsiung Journal of Medical Sciences

DT Journal

LA English

AB To establish a sensitive, specific and reproducible PCR assay for the detection of ***Mycobacterium*** tuberculosis, we evaluated three target DNAs: IS6110, 65 kDa heat shock protein gene; and mtp40 genomic fragment. We purified genomic DNA from 15 ***mycobacterial*** strains including four *M. tuberculosis* isolates, four *M. bovis* BCG isolates, and one of each for *M. fortuitum*, *M. avium*, *M. intracellulare*, *M. szulgai*, *M.*

scrofulaceum, M. chelonae, and M. goodii from the culture and used them as the template DNA. We studied 3 ***primer*** sets for IS6110, 2 ***primer*** sets for 65 kDa heat shock protein gene, and 3 ***primer*** sets for mtp40. Depending on the assay, these ***primer*** sets were used in the single-step PCR and/or nested PCR.

The PCR assay targeting the 65 kDa protein gene could detect all of the tested ***mycobacterial*** strains, whereas targeting the IS6110 sequence resulted in detection of only M. tuberculosis and M. bovis BCG. Furthermore, targeting the mtp40 genomic fragment could be used to distinguish M. tuberculosis from M. bovis BCG. Using a nested PCR assay with ***primer*** sets specifically targeting the IS6110 or 65 kDa, we have been able to detect single copy M. tuberculosis genomic DNA. When the mtp40 genomic fragment was used as the target DNA, the sensitivity of detection was 10 copies of M. tuberculosis genomic DNA. This assay was demonstrated to have good sensitivity and specificity for detection and discrimination of ***mycobacterial*** species, and could be used in analyzing the clin. samples with low copy no. infections such as the cerebrospinal fluid from the patient with tuberculous meningitis.

RE.CNT 25 THERE ARE 25 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

TI Determination of the sensitivity and specificity of PCR assays using different target DNAs for the detection of ***Mycobacterium*** tuberculosis

AB To establish a sensitive, specific and reproducible PCR assay for the detection of ***Mycobacterium*** tuberculosis, we evaluated three target DNAs: IS6110, 65 kDa heat shock protein gene; and mtp40 genomic fragment. We purified genomic DNA from 15 ***mycobacterial*** strains including four M. tuberculosis isolates, four M. bovis BCG isolates, and one of each for M. fortuitum, M. avium, . . . M. scrofulaceum, M. chelonae, and M. goodii from the culture and used them as the template DNA. We studied 3 ***primer*** sets for IS6110, 2 ***primer*** sets for 65 kDa heat shock protein gene, and 3 ***primer*** sets for mtp40. Depending on the assay, these ***primer*** sets were used in the single-step PCR and/or nested PCR. The PCR assay targeting the 65 kDa protein gene could detect all of the tested ***mycobacterial*** strains, whereas targeting the IS6110 sequence resulted in detection of only M. tuberculosis and M. bovis BCG. Furthermore, targeting the . . . mtp40 genomic fragment could be used to distinguish M. tuberculosis from M. bovis BCG. Using a nested PCR assay with ***primer*** sets specifically targeting the IS6110 or 65 kDa, we have been able to detect single copy M. tuberculosis genomic DNA. . . . of M. tuberculosis genomic DNA. This assay was demonstrated to have good sensitivity and specificity for detection and discrimination of ***mycobacterial*** species, and could be used in analyzing the clin. samples with low copy no. infections such as the cerebrospinal fluid. . .

ST PCR ***Mycobacterium*** tuberculosis detection IS6110 mtp40
hsp65

IT Heat-shock proteins
RL: BSU (Biological study, unclassified); BIOL (Biological study) (HSP 65, gene for; detn. of sensitivity and specificity of PCR assays using different target DNAs for detection of ***Mycobacterium*** tuberculosis)

IT Insertion sequence
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study) (IS6110; detn. of sensitivity and specificity of PCR assays using different target DNAs for detection of ***Mycobacterium***

tuberculosis)

IT ***Mycobacterium*** tuberculosis
 PCR (polymerase chain reaction)
 (detrn. of sensitivity and specificity of PCR assays using different
 target DNAs for detection of ***Mycobacterium*** tuberculosis)

IT ***Primers*** (nucleic acid)
 RL: ARG (Analytical reagent use); PRP (Properties); ANST (Analytical
 study); USES (Uses)
 (detrn. of sensitivity and specificity of PCR assays using different
 target DNAs for detection of ***Mycobacterium*** tuberculosis)

IT ***Diagnosis***
 (mol.; detrn. of sensitivity and specificity of PCR assays using
 different target DNAs for detection of ***Mycobacterium***
 tuberculosis)

IT Gene, microbial
 RL: BSU (Biological study, unclassified); PRP (Properties); BIOL
 (Biological study)
 (mtp40; detrn. of sensitivity and specificity of PCR assays using
 different target DNAs for detection of ***Mycobacterium***
 tuberculosis)

IT 256216-29-2 256216-30-5 256216-31-6 256216-32-7
 RL: ARG (Analytical reagent use); PRP (Properties); ANST (Analytical
 study); USES (Uses)
 (PCR ***primer*** for IS6110; detrn. of sensitivity and specificity
 of PCR assays using different target DNAs for detection of
 Mycobacterium tuberculosis)

IT 256216-33-8 256216-34-9 256216-35-0 256216-36-1
 RL: ARG (Analytical reagent use); PRP (Properties); ANST (Analytical
 study); USES (Uses)
 (PCR ***primer*** for mtp40; detrn. of sensitivity and specificity
 of PCR assays using different target DNAs for detection of
 Mycobacterium tuberculosis)

L9 ANSWER 51 OF 71 CAPLUS COPYRIGHT 2009 ACS on STN
 AN 1999:436334 CAPLUS <<LOGINID::20090617>>
 DN 131:253056

TI Characterization to species level of clinical isolates of the
 Mycobacterium avium complex by DNA probes, DT1-DT6 PCR and
 PCR-restriction enzyme analysis

AU Garriga, Xavier; Cortes, Pilar; March, Francesca; Rodriguez, Purificacion;
 Garrigo, Montserrat; Moreno, Carmen; Garcia, Elena; Coll, Pere; Prats,
 Guillem

CS Servei de Microbiologia, Hospital de la Santa Creu i Sant Pau, Barcelona,
 08025, Spain

SO Clinical Microbiology and Infection (1999), 5(6), 379-382
 CODEN: CMINFM; ISSN: 1198-743X

PB Decker Europe
 DT Journal
 LA English

AB The AccuProbe System was used to classify clin. isolates of M. avium and
 M. intracellulare. ***Primers*** were used to amplify specific DNA
 fragments (DT1-DT6) for ***identification*** of these isolates by PCR.
 In addn., PCR-restriction enzyme anal. (PRA) was performed on these
 strains based on ***primers*** amplifying a fragment of the gene
 hsp65. PRA was more sensitive than the AccuProbe System and
 DT1-DT6 amplification.

RE.CNT 23 THERE ARE 23 CITED REFERENCES AVAILABLE FOR THIS RECORD

ALL CITATIONS AVAILABLE IN THE RE FORMAT

- TI Characterization to species level of clinical isolates of the
 Mycobacterium avium complex by DNA probes, DT1-DT6 PCR and
 PCR-restriction enzyme analysis
- AB The AccuProbe System was used to classify clin. isolates of *M. avium* and
M. intracellulare. ***Primers*** were used to amplify specific DNA
 fragments (DT1-DT6) for ***identification*** of these isolates by PCR.
 In addn., PCR-restriction enzyme anal. (PRA) was performed on these
 strains based on ***primers*** amplifying a fragment of the gene
 hsp65. PRA was more sensitive than the AccuProbe System and
 DT1-DT6 amplification.
- ST ***Mycobacterium*** ***diagnosis*** probe restriction enzyme PCR
- IT Nucleic acid hybridization
 (DNA-DNA; characterization to species level of clin. isolates of
 Mycobacterium avium complex by DNA probes, DT1-DT6 PCR and
 PCR-restriction enzyme anal.)
- IT Heat-shock proteins
 RL: ADV (Adverse effect, including toxicity); ARU (Analytical role,
 unclassified); ANST (Analytical study); BIOL (Biological study)
 (HSP 65; characterization to species level of clin. isolates of
 Mycobacterium avium complex by DNA probes, DT1-DT6 PCR and
 PCR-restriction enzyme anal.)
- IT ***Diagnosis***
 Mycobacterium avium
 Mycobacterium intracellulare
 PCR (polymerase chain reaction)
 (characterization to species level of clin. isolates of
 Mycobacterium avium complex by DNA probes, DT1-DT6 PCR and
 PCR-restriction enzyme anal.)
- IT Probes (nucleic acid)
 RL: ARG (Analytical reagent use); THU (Therapeutic use); ANST (Analytical
 study); BIOL (Biological study); USES (Uses)
 (characterization to species level of clin. isolates of
 Mycobacterium avium complex by DNA probes, DT1-DT6 PCR and
 PCR-restriction enzyme anal.)
- IT Gene, microbial
 RL: ADV (Adverse effect, including toxicity); ANT (Analyte); ANST
 (Analytical study); BIOL (Biological study)
 (***hsp65*** ; characterization to species level of clin. isolates
 of ***Mycobacterium*** avium complex by DNA probes, DT1-DT6 PCR and
 PCR-restriction enzyme anal.)
- IT 81295-18-3 93229-61-9, Restriction endonuclease BstEII 148908-88-7,
 DNA, d(C-G-T-T-C-G-A-T-C-G-C-A-G-T-T-T-G-C-A-G-C-G-C-G-T-A-C-A)
 148908-89-8, DNA, d(A-T-G-G-C-C-G-G-G-A-G-A-C-G-A-T-C-T-A-T-G-C-C-G-G-C-G-
 T-A-C) 150951-89-6 150951-90-9
 RL: ARG (Analytical reagent use); THU (Therapeutic use); ANST (Analytical
 study); BIOL (Biological study); USES (Uses)
 (characterization to species level of clin. isolates of
 Mycobacterium avium complex by DNA probes, DT1-DT6 PCR and
 PCR-restriction enzyme anal.)
- L9 ANSWER 52 OF 71 CAPLUS COPYRIGHT 2009 ACS on STN
- AN 1999:370904 CAPLUS <<LOGINID::20090617>>
- DN 131:180372
- TI Species-specific ***identification*** of ***Mycobacterium***
leprae by PCR-restriction fragment length polymorphism analysis of the
 hsp65 gene

AU Rastogi, Nalin; Goh, Khye Seng; Berchel, Mylene
 CS Unite de la Tuberculose et des Mycobacteries, Institut Pasteur, Pointe a
 Pitre, 97165, Guadeloupe
 SO Journal of Clinical Microbiology (1999), 37(6), 2016-2019
 CODEN: JCMIDW; ISSN: 0095-1137
 PB American Society for Microbiology
 DT Journal
 LA English
 AB PCR-restriction fragment length polymorphism anal. (PRA) of the
 hsp65 gene present in all ***mycobacteria*** was used in the
 present investigation to characterize ***Mycobacterium*** leprae.
 Bacilli were extd. and purified from different organs from exptl. infected
 armadillos and nude mice (Swiss mice of nu/nu origin). A total of 15
 samples were assayed in duplicate, and the results were compared with
 those obtained for a total of 147 cultivable ***mycobacteria***
 representing 34 species. Irresp. of its origin or viability, M. leprae
 strains from all the samples were uniformly characterized by two fragments
 of 315 and 135 bp upon BstEII digestion and two fragments of 265 and 130
 bp upon HaeIII digestion. PRA is a relatively simple method and permits
 the conclusive ***identification*** of M. leprae to the species level.
 RE.CNT 15 THERE ARE 15 CITED REFERENCES AVAILABLE FOR THIS RECORD
 ALL CITATIONS AVAILABLE IN THE RE FORMAT
 TI Species-specific ***identification*** of ***Mycobacterium***
 leprae by PCR-restriction fragment length polymorphism analysis of the
 hsp65 gene
 AB PCR-restriction fragment length polymorphism anal. (PRA) of the
 hsp65 gene present in all ***mycobacteria*** was used in the
 present investigation to characterize ***Mycobacterium*** leprae.
 Bacilli were extd. and purified from different organs from exptl. infected
 armadillos and nude mice (Swiss mice of nu/nu. . . 15 samples were
 assayed in duplicate, and the results were compared with those obtained
 for a total of 147 cultivable ***mycobacteria*** representing 34
 species. Irresp. of its origin or viability, M. leprae strains from all
 the samples were uniformly characterized by. . . two fragments of 265
 and 130 bp upon HaeIII digestion. PRA is a relatively simple method and
 permits the conclusive ***identification*** of M. leprae to the
 species level.
 ST PCR RFLP ***Mycobacterium*** species ***identification***
 hsp65
 IT ***Primers*** (nucleic acid)
 Primers (nucleic acid)
 RL: ARG (Analytical reagent use); BSU (Biological study, unclassified);
 PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES
 (Uses)
 (DNA; species-specific ***identification*** of
 Mycobacterium leprae by PCR-restriction fragment length
 polymorphism anal. of ***hsp65*** gene)
 IT Gene, microbial
 RL: ANT (Analyte); BSU (Biological study, unclassified); ANST (Analytical
 study); BIOL (Biological study)
 (***hsp65*** ; species-specific ***identification*** of
 Mycobacterium leprae by PCR-restriction fragment length
 polymorphism anal. of ***hsp65*** gene)
 IT DNA
 DNA
 RL: ARG (Analytical reagent use); BSU (Biological study, unclassified);
 PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES

(Uses)
 (***primer*** ; species-specific ***identification*** of
 Mycobacterium leprae by PCR-restriction fragment length
 polymorphism anal. of ***hsp65*** gene)

IT DNA sequences
 (***primers*** ; species-specific ***identification*** of
 Mycobacterium leprae by PCR-restriction fragment length
 polymorphism anal. of ***hsp65*** gene)

IT ***Mycobacterium*** leprae
 PCR (polymerase chain reaction)
 RFLP (restriction fragment length polymorphism)
 (species-specific ***identification*** of ***Mycobacterium***
 leprae by PCR-restriction fragment length polymorphism anal. of
 hsp65 gene)

IT 1509b1-89-6
 RL: ARG (Analytical reagent use); BSU (Biological study, unclassified);
 PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES
 (Uses)
 (nucleotide sequence of useful ***primer*** Tbl1; species-specific
 identification of ***Mycobacterium*** leprae by
 PCR-restriction fragment length polymorphism anal. of ***hsp65***
 gene)

IT 1509b1-90-9
 RL: ARG (Analytical reagent use); BSU (Biological study, unclassified);
 PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES
 (Uses)
 (nucleotide sequence of useful ***primer*** Tbl2; species-specific
 identification of ***Mycobacterium*** leprae by
 PCR-restriction fragment length polymorphism anal. of ***hsp65***
 gene)

IT 8129b-18-3 93229-61-9, Restriction endonuclease bsteii
 RL: ARG (Analytical reagent use); BSU (Biological study, unclassified);
 PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES
 (Uses)
 (species-specific ***identification*** of ***Mycobacterium***
 leprae by PCR-restriction fragment length polymorphism anal. of
 hsp65 gene)

L9 ANSWER 53 OF 71 CAPLUS COPYRIGHT 2009 ACS on STN
 AN 1999:200588 CAPLUS <<LOGINID:20090617>>
 DN 131:68708
 TI Polymerase chain reaction, with sequencing, as a ***diagnostic*** tool
 in culture-negative bacterial meningitis

AU Dicuonzo, Giordano; Lorino, Giulia; Lilli, Daniela; Rivanera, Daniela;
 Guarino, Paola; Angeletti, Silvia; Gherardi, Giovanni; Filadoro, Francesco

CS Libera Università, Campus Bio-Medico, Facoltà Medicina e Chirurgia,
 Università "La Sapienza", Rome, 83-00155, Italy

SO Clinical Microbiology and Infection (1999), 5(2), 92-96
 CODEN: CMINFM; ISSN: 1198-743X

PB Decker Europe
 DT Journal
 LA English

AB To evaluate the feasibility of using 16S rDNA universal ***primer***
 PCR (followed by sequencing) and 65-kDa heat shock ***Mycobacterium***
 tuberculosis protein gene PCR as a method to det. a bacterial etiol. in
 culture-neg. cerebrospinal fluid (CSF) samples. One hundred and
 forty-nine CSF samples from 128 patients were processed. DNA was extd.

from the CSF samples and amplified with the eubacterial 16S rDNA
 primers P11E and P13B, and with the 65-kDa heat shock protein
 gene

mycobacterial ***primers*** . The amplicons were
 identified by sequencing and specific oligoprobe hybridization.
 Overall, a microbiol. ***diagnosis*** was made in 11 of 125 ultimately
 culture-neg. cases. The use of 65-kDa heat shock protein gene PCR was
 needed to improve the ***diagnosis*** of tuberculous meningitis; in
 four patients, prospectively studied, the outcome of antituberculous
 therapy could also be followed. In culture-neg. bacterial meningitis it
 is possible to improve the microbiol. ***diagnosis*** by use of 16S
 rDNA amplification and sequencing, together with amplification of a more
 specific gene in ***mycobacteria*** .

RE.CNT 18 THERE ARE 18 CITED REFERENCES AVAILABLE FOR THIS RECORD
 ALL CITATIONS AVAILABLE IN THE RE FORMAT

TI Polymerase chain reaction, with sequencing, as a ***diagnostic*** tool
 in culture-negative bacterial meningitis

AB To evaluate the feasibility of using 16S rDNA universal ***primer***
 PCR (followed by sequencing) and 65-kDa heat shock ***Mycobacterium***
 tuberculosis protein gene PCR as a method to det. a bacterial etiol. in
 culture-neg. cerebrospinal fluid (CSF) samples. One hundred. . .
 samples from 128 patients were processed. DNA was extd. from the CSF
 samples and amplified with the eubacterial 16S rDNA ***primers*** P11E
 and P13B, and with the 65-kDa heat shock protein gene
 mycobacterial ***primers*** . The amplicons were
 identified by sequencing and specific oligoprobe hybridization.
 Overall, a microbiol. ***diagnosis*** was made in 11 of 125 ultimately
 culture-neg. cases. The use of 65-kDa heat shock protein gene PCR was
 needed to improve the ***diagnosis*** of tuberculous meningitis; in
 four patients, prospectively studied, the outcome of antituberculous
 therapy could also be followed. In culture-neg. bacterial meningitis it
 is possible to improve the microbiol. ***diagnosis*** by use of 16S
 rDNA amplification and sequencing, together with amplification of a more
 specific gene in ***mycobacteria*** .

ST PCR 16S rDNA ***HSP65*** ***diagnosis*** tuberculous meningitis
 IT rRNA

RL: BSU (Biological study, unclassified); BIOL (Biological study)
 (16 S; PCR using 16S rDNA and ***HSP65*** protein ***primers***
 of DNA from cerebrospinal fluid in ***diagnosis*** of culture-neg.
 tuberculous meningitis in humans)

IT ***Primers*** (nucleic acid)
 Primers (nucleic acid)

RL: ARG (Analytical reagent use); THU (Therapeutic use); ANST (Analytical
 study); BIOL (Biological study); USES (Uses)
 (DNA; PCR using 16S rDNA and ***HSP65*** protein ***primers***
 of DNA from cerebrospinal fluid in ***diagnosis*** of culture-neg.
 tuberculous meningitis in humans)

IT Heat-shock proteins

RL: BSU (Biological study, unclassified); BIOL (Biological study)
 (HSP 65; PCR using 16S rDNA and ***HSP65*** protein ***primers***
 of DNA from cerebrospinal fluid in ***diagnosis*** of culture-neg.
 tuberculous meningitis in humans)

IT Gene, animal

RL: ANT (Analyte); THU (Therapeutic use); ANST (Analytical study); BIOL
 (Biological study); USES (Uses)
 (***HSP65*** ; PCR using 16S rDNA and ***HSP65*** protein
 primers of DNA from cerebrospinal fluid in ***diagnosis***

of culture-neg. tuberculous meningitis in humans)

IT ***Mycobacterium*** tuberculosis
 PCR (polymerase chain reaction)
 (PCR using 16S rDNA and ***HSP65*** protein ***primers*** of
 DNA from cerebrospinal fluid in ***diagnosis*** of culture-neg.
 tuberculous meningitis in humans)

IT ***Diagnosis***
 (mol.; PCR using 16S rDNA and ***HSP65*** protein ***primers***
 of DNA from cerebrospinal fluid in ***diagnosis*** of culture-neg.
 tuberculous meningitis in humans)

IT DNA
 DNA
 RL: ARG (Analytical reagent use); THU (Therapeutic use); ANST (Analytical
 study); BIOL (Biological study); USES (Uses)
 (***primer*** ; PCR using 16S rDNA and ***HSP65*** protein
 primers of DNA from cerebrospinal fluid in ***diagnosis***
 of culture-neg. tuberculous meningitis in humans)

IT DNA
 RL: ANT (Analyte); THU (Therapeutic use); ANST (Analytical study); BIOL
 (Biological study); USES (Uses)
 (rDNA, 16 S; PCR using 16S rDNA and ***HSP65*** protein
 primers of DNA from cerebrospinal fluid in ***diagnosis***
 of culture-neg. tuberculous meningitis in humans)

IT Meningitis
 (tuberculous; PCR using 16S rDNA and ***HSP65*** protein
 primers of DNA from cerebrospinal fluid in ***diagnosis***
 of culture-neg. tuberculous meningitis in humans)

L9 ANSWER 54 OF 71 CAPLUS COPYRIGHT 2009 ACS on STN
 AN 1999:173164 CAPLUS <<LOGINID:20090617>>
 DN 131:68653
 TI ***hsp65*** Sequencing for ***identification*** of rapidly growing
 mycobacteria

AU Ringuet, H.; Akoua-Koffi, C.; Honore, S.; Varnerot, A.; Vincent, V.;
 Berche, P.; Gaillard, J. L.; Pierre-Audigier, C.
 CS Service de Microbiologie, Hopital Necker-Enfants Malades, Paris, 75015,
 Fr.

SO Journal of Clinical Microbiology (1999), 37(3), 852-857
 CODEN: JCMIDW; ISSN: 0095-1137

PB American Society for Microbiology
 DT Journal
 LA English

AB Partial sequencing of the ***hsp65*** gene was used for the
 identification of rapidly growing ***mycobacteria*** (RGM).

A
 441-bp fragment (A. Telenti, F. Marchesi, M. Balz, F. Bally, E. Bottger,
 and T. Bodmer, J. Clin. Microbiol. 31:175-178, 1993) was amplified and
 sequenced by an automated fluorescence-based method involving capillary
 electrophoresis. Type strains of 10 RGM species were first studied. Each
 species had a unique nucleotide sequence, distinguishing it clearly from
 the other species. A panel of strains from the four main RGM species
 responsible for human infections, ***Mycobacterium*** abscessus, and
 Mycobacterium chelonae, ***Mycobacterium*** fortuitum, and
 Mycobacterium peregrinum, was also studied. There were few
 sequence differences within each of these species (<2% of bases were
 different from the type strain sequence), and they had no effect on
 species assignment. ***Hsp65*** sequencing unambiguously

differentiated *M. chelonae* and *M. abscessus*, two species difficult to
 identify by classical methods and 16S rRNA gene sequencing. The
 devised procedure is a rapid and reliable tool for the
 identification of RGM species.

RE.CNT 24 THERE ARE 24 CITED REFERENCES AVAILABLE FOR THIS RECORD
 ALL CITATIONS AVAILABLE IN THE RE FORMAT

TI ***hsp65*** Sequencing for ***identification*** of rapidly growing
 mycobacteria

AB Partial sequencing of the ***hsp65*** gene was used for the
 identification of rapidly growing ***mycobacteria*** (RGM).

A
 441-bp fragment (A. Telenti, F. Marchesi, M. Balz, F. Bally, E. Bottger,
 and T. Bodmer, J. Clin. Microbiol. . . . it clearly from the other
 species. A panel of strains from the four main RGM species responsible
 for human infections, ***Mycobacterium*** abscessus,
 Mycobacterium chelonae, ***Mycobacterium*** fortuitum, and
 Mycobacterium peregrinum, was also studied. There were few
 sequence differences within each of these species (<2% of bases were
 different from the type strain sequence), and they had no effect on
 species assignment. ***Hsp65*** sequencing unambiguously
 differentiated *M. chelonae* and *M. abscessus*, two species difficult to
 identify by classical methods and 16S rRNA gene sequencing. The
 devised procedure is a rapid and reliable tool for the
 identification of RGM species.

ST ***Mycobacterium*** species ***identification*** sequencing
 hsp65 gene

IT DNA sequence analysis
 DNA sequences
 Mycobacterium
 Mycobacterium abscessus
 Mycobacterium chelonae
 Mycobacterium fortuitum
 Mycobacterium peregrinum

PCR (polymerase chain reaction)
 (***hsp65*** Sequencing for ***identification*** of rapidly
 growing ***mycobacteria***)

IT Gene, microbial
 RL: ANT (Analyte); PRP (Properties); ANST (Analytical study)
 (***hsp65*** ; ***hsp65*** Sequencing for ***identification***
 of rapidly growing ***mycobacteria***)

IT 228573-12-4
 RL: ARG (Analytical reagent use); PRP (Properties); THU (Therapeutic use);
 ANST (Analytical study); BIOL (Biological study); USES (Uses)
 (PCR ***primer*** Tbl1; ***hsp65*** Sequencing for
 identification of rapidly growing ***mycobacteria***)

IT 228573-13-5
 RL: ARG (Analytical reagent use); PRP (Properties); THU (Therapeutic use);
 ANST (Analytical study); BIOL (Biological study); USES (Uses)
 (PCR ***primer*** Tbl2; ***hsp65*** Sequencing for
 identification of rapidly growing ***mycobacteria***)

IT 224287-13-2 224287-18-7 225760-17-8 229016-49-3 229016-50-6
 229016-51-7 229016-52-8 229016-53-9 229016-54-0 229016-56-2
 229016-57-3
 RL: ANT (Analyte); BUU (Biological use, unclassified); PRP (Properties);
 ANST (Analytical study); BIOL (Biological study); USES (Uses)
 (nucleotide sequence; ***hsp65*** Sequencing for
 identification of rapidly growing ***mycobacteria***)

L9 ANSWER 55 OF 71 CAPLUS COPYRIGHT 2009 ACS ON STN
 AN 1997:723093 CAPLUS <<LOGINID::20090617>>
 DN 128:30784
 QREF 128:5933a,5936a
 TI Rapid ***identification*** of ***mycobacteria*** to species level
 by PCR-restriction fragment length polymorphism analysis of the
 hsp65 gene and proposition of an algorithm to differentiate 34
 mycobacterial species
 AU Devallois, Anne; Goh, Khye Seng; Rastogi, Nalin
 CS Unite de la Tuberculose et des Mycobacteries, Institut Pasteur, Pointe a
 Pitre, 97165, Guadeloupe
 SO Journal of Clinical Microbiology (1997), 35(11), 2969-2973
 CODEN: JCMIDW; ISSN: 0095-1137
 PB American Society for Microbiology
 DT Journal
 LA English
 AB PCR-restriction fragment length polymorphism anal. (PRA) of the
 hsp65 gene was applied to 108 ***mycobacterial*** isolates
 representing 34 species to evaluate its potential as a rapid ref. method.
 A total of 49 distinct patterns were obtained; 25 species were
 characterized by a single PRA pattern, while 9 species gave more than one
 specific pattern. An algorithm describing these 34 species (which
 includes five addnl. species and new subgroups of ***Mycobacterium***
 kansasii, M. abscessus, and M. peregrinum) is proposed. A relatively
 simple and inexpensive method, PRA may be particularly helpful in routine
 clin. microbiol. labs.
 TI Rapid ***identification*** of ***mycobacteria*** to species level
 by PCR-restriction fragment length polymorphism analysis of the
 hsp65 gene and proposition of an algorithm to differentiate 34
 mycobacterial species
 AB PCR-restriction fragment length polymorphism anal. (PRA) of the
 hsp65 gene was applied to 108 ***mycobacterial*** isolates
 representing 34 species to evaluate its potential as a rapid ref. method.
 A total of 49 distinct patterns were. . . more than one specific
 pattern. An algorithm describing these 34 species (which includes five
 addnl. species and new subgroups of ***Mycobacterium*** kansasii, M.
 abscessus, and M. peregrinum) is proposed. A relatively simple and
 inexpensive method, PRA may be particularly helpful in. . .
 ST PCR RFLP ***identification*** taxonomy ***Mycobacterium***
 IT Gene, microbial
 RL: ANT (Analyte); BSU (Biological study, unclassified); ANST (Analytical
 study); BIOL (Biological study)
 (***hsp65*** ; ***identification*** of ***mycobacteria*** to
 species level by ***hsp65*** gene PCR-RFLP proposal of algorithm
 differentiating 34 ***mycobacterial*** species)
 IT ***Mycobacterium***
 PCR (polymerase chain reaction)
 RFLP (restriction fragment length polymorphism)
 Taxonomy
 (***identification*** of ***mycobacteria*** to species level by
 hsp65 gene PCR-RFLP proposal of algorithm differentiating 34
 mycobacterial species)
 IT 150951-89-6 150951-90-9
 RL: ARG (Analytical reagent use); BUU (Biological use, unclassified); ANST
 (Analytical study); BIOL (Biological study); USES (Uses)
 (***primer*** Tbl1; ***identification*** of

mycobacteria to species level by ***hsp65*** gene PCR-RFLP
 proposal of algorithm differentiating 34 ***mycobacterial***
 species)

L9 ANSWER 56 OF 71 CAPLUS COPYRIGHT 2009 ACS on STN

AN 1997:36419 CAPLUS <LOGINID:20090617>>

DN 126:70783

OREF 126:13605a,13608a

TI ***Identification*** and subspecific differentiation of
 Mycobacterium scrofulaceum by automated sequencing of a region of
 the gene (***hsp65***) encoding a 65-kilodalton heat shock protein

AU Swanson, Douglas S.; Pan, Xi; Musser, James M.

CS Section of Infectious Diseases, Department of Pediatrics, Baylor College
 of Medicine, Houston, TX, 77030, USA

SO Journal of Clinical Microbiology (1996), 34(12), 3151-3159

CODEN: JCMIDW; ISSN: 0095-1137

PB American Society for Microbiology

DT Journal

LA English

AB ***Mycobacterium*** scrofulaceum is most commonly recovered from
 children with cervical lymphadenitis, although it also accounts for
 approx. 2% of the ***mycobacterial*** infections in AIDS patients.
 Species assignment of M. scrofulaceum isolates by conventional techniques
 can be difficult and time-consuming. To develop a strategy for rapid
 species assignment of these organisms, a 360-bp region of the gene (
 hsp65) encoding a 65-kDa heat shock protein in 37 isolates from
 diverse sources was sequenced. Eight ***hsp65*** alleles were
 identified, and these sequences formed phylogenetic clusters and
 lineages largely distinct from other ***Mycobacterium*** species.
 There was incomplete correlation between serovar designation and
 hsp65 allele assignment. The ***hsp65*** data correlated
 strongly with the results of sequence anal. of the gene coding for 16S
 rRNA. Automated DNA sequencing of a 360-bp region of the ***hsp65***
 gene provides a rapid and unambiguous method for species assignment of
 these acid-fast organisms for ***diagnostic*** purposes.

TI ***Identification*** and subspecific differentiation of
 Mycobacterium scrofulaceum by automated sequencing of a region of
 the gene (***hsp65***) encoding a 65-kilodalton heat shock protein

AB ***Mycobacterium*** scrofulaceum is most commonly recovered from
 children with cervical lymphadenitis, although it also accounts for
 approx. 2% of the ***mycobacterial*** infections in AIDS patients.
 Species assignment of M. scrofulaceum isolates by conventional techniques
 can be difficult and time-consuming. To develop a strategy for rapid
 species assignment of these organisms, a 360-bp region of the gene (
 hsp65) encoding a 65-kDa heat shock protein in 37 isolates from
 diverse sources was sequenced. Eight ***hsp65*** alleles were
 identified, and these sequences formed phylogenetic clusters and
 lineages largely distinct from other ***Mycobacterium*** species.
 There was incomplete correlation between serovar designation and
 hsp65 allele assignment. The ***hsp65*** data correlated
 strongly with the results of sequence anal. of the gene coding for 16S
 rRNA. Automated DNA sequencing of a 360-bp region of the ***hsp65***
 gene provides a rapid and unambiguous method for species assignment of
 these acid-fast organisms for ***diagnostic*** purposes.

ST sequencing gene ***hsp65*** typing taxonomy ***Mycobacterium*** ;

diagnosis ***Mycobacterium*** gene ***hsp65*** sequencing

IT Gene, microbial

RL: ANT (Analyte); BSU (Biological study, unclassified); PRP (Properties);
 ANST (Analytical study); BIOL (Biological study)
 (***hsp65*** ; ***identification*** and differentiation of
 Mycobacterium scrofulaceum by automated sequencing gene
 hsp65 region encoding 65-kDa heat shock protein)

IT DNA sequence analysis
 DNA sequences
 Mycobacterium scrofulaceum
 Protein sequences
 Taxonomy
 (***identification*** and differentiation of ***Mycobacterium***
 scrofulaceum by automated sequencing gene ***hsp65*** region
 encoding 65-kDa heat shock protein)

IT 150951-89-6 150951-90-9
 RL: ARG (Analytical reagent use); THU (Therapeutic use); ANST (Analytical
 study); BIOL (Biological study); USES (Uses)
 (***primer*** ; ***identification*** and differentiation of
 Mycobacterium scrofulaceum by automated sequencing gene
 hsp65 region encoding 65-kDa heat shock protein)

L9 ANSWER 57 OF 71 EMBASE COPYRIGHT (c) 2009 Elsevier B.V. All rights
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AN 2007263708 EMBASE <<LOGINID::20090617>>

TI Application of restriction enzyme analysis technique based on 65kDa heat
 shock protein gene for fingerprinting and differentiation of
 Mycobacterium tuberculosis clinical strains isolated from
 tuberculosis patients in Ahwaz, Iran.

AU Khosravi, Azar D., Dr. (correspondence); Hashemi, Abdulrazagh
 CS Dept. of Microbiology, School of Medicine, Ahwaz Jondi Shapour University
 of Medical Sciences, Ahwaz, Iran, Islamic Republic of. khosravi.az@yahoo.co
 m

SO Pakistan Journal of Medical Sciences, (Apr 2007) Vol. 23, No. 2, pp.
 216-219.
 Refs: 14
 ISSN: 1682-024X CODEN: PJMSC6

CY Pakistan
 DT Journal; Article

FS 015 Chest Diseases, Thoracic Surgery and Tuberculosis
 004 Microbiology: Bacteriology, Mycology, Parasitology and Virology

LA English
 SL English
 ED Entered STN: 21 Jun 2007
 Last Updated on STN: 21 Jun 2007

AB Objective: Application of ***identification*** methodology of
 restriction enzyme analysis (REA) for fingerprinting of the expanded
 population of ***Mycobacterium*** tuberculosis (MTB) isolates.
 Methodology: A total of 150 clinical isolates from patients referred to TB
 reference laboratory, Public Health Centre, Ahwaz, Iran, were
 identified as MTB by using conventional culture and biochemical
 tests from January to December 2004. The PCR-REA method uses a PCR step
 based on amplification of a 439 bp fragment of ***hsp65*** gene
 involving genus specific ***primers*** and restriction enzyme analysis
 by digestion of products with HaeIII & BstEII enzymes were employed.
 Results: The identical restriction patterns similar to MTB reference
 strains equal to 160/145/72bp fragments for Hae III and 250/120/82bp
 fragments for Bst EII digests were seen in 145 isolates (96.6%). The
 diverse patterns were observed for five isolates in Hae III digest as

180/100/80 bp, 194/72 bp and 160/145 bp representing the possible intra-species variation within studied MTB strains , while their Bst EII digestion patterns showed no variation. Conclusions: The PCR-REA technique revealed three different new patterns for Hae III digest. However to verify that they are indeed MTB isolates, a sequence-based analysis of the exceptional isolates should be performed.

TI Application of restriction enzyme analysis technique based on 65kDa heat shock protein gene for fingerprinting and differentiation of
 Mycobacterium tuberculosis clinical strains isolated from tuberculosis patients in Ahwaz, Iran.

AB Objective: Application of ***identification*** methodology of restriction enzyme analysis (REA) for fingerprinting of the expanded population of ***Mycobacterium*** tuberculosis (MTB) isolates. Methodology: A total of 150 clinical isolates from patients referred to TB reference laboratory, Public Health Centre, Ahwaz, Iran, were
 identified as MTB by using conventional culture and biochemical tests from January to December 2004. The PCR-REA method uses a PCR step based on amplification of a 439 bp fragment of ***hsp65*** gene involving genus specific ***primers*** and restriction enzyme analysis by digestion of products with HaeIII & BstEII enzymes were employed. Results: The identical restriction patterns. . .

CT Medical Descriptors:
 adult
 aged
 article
 bacterial strain
 bacterium culture
 bacterium isolate
 biochemistry
 controlled study
 *DNA fingerprinting
 DNA sequence
 female
 genetic variability
 human
 intraspecific variation
 Iran
 laboratory
 *lung tuberculosis: ET, etiology
 male
 Mycobacterium tuberculosis
 nonhuman
 *polymerase chain reaction
 *restriction mapping
 *tuberculosis: ET, etiology
 *heat shock protein 65

L9 ANSWER 58 OF 71 MEDLINE on STN
 AN 2008153624 MEDLINE <<LOGINID:20090617>>
 DN PubMed ID: 18310283
 TI A novel vaccine targeting gastrin-releasing peptide: efficient inhibition of breast cancer growth in vivo.
 AU Guojun Wu; Wei Guo; Kedong Ouyan; Yi He; Yanfei Xie; Qingmei Chen; Yankai Zhang; Jie Wu; Hao Fan; Taiming Li; Jingjing Liu; Rongyue Cao
 CS Minigene Pharmacy Laboratory of the Biopharmaceutical College, China Pharmaceutical University, Nanjing, PR China.
 SO Endocrine-related cancer, (2008 Mar) Vol. 15, No. 1, pp. 149-59.

Journal code: 9436481. ISSN: 1351-0088.

CY England: United Kingdom

DT Journal; Article; (JOURNAL ARTICLE)
(RESEARCH SUPPORT, NON-U.S. GOV'T)

LA English

FS Priority Journals

EM 200805

ED Entered STN: 4 Mar 2008

Last Updated on STN: 9 May 2008

Entered Medline: 8 May 2008

AB Gastrin-releasing peptide (GRP), a bombesin-like peptide, is an autocrine growth factor that can stimulate the growth of various cancer cells. We developed a novel protein vaccine ***HSP65*** -(GRP-10)(6) (HG6) that consists of six copies of a 10-amino acid residue epitope of GRP C-terminal fragment carried by ***mycobacterial*** 65 kDa ***HSP65*** and then immunized mice via subcutaneous injection. Strong humoral and cell-mediated immune responses were induced. High titer of anti-GRP antibodies was detected in immunized mice sera by ELISA and verified by Western blot analysis. Activity of CD4+T lymphocytes, especially high levels of interferon (INF)-gamma, were developed in mice immunized with HG6 when compared with ***HSP65*** or PBS. We found that immunogene tumor therapy with a vaccine based on GRP was effective at both protective and therapeutic antitumor immunity in breast tumor models in mice. The purified GRP monoclonal antibody (McAb) was proved to be potential in inhibiting EMT-6 tumor cell proliferation in vitro. The attenuation induced by active immune responses on tumor-induced angiogenesis was observed with an intradermal tumor model in mice. Taken together, we demonstrate for the first time that immune responses that are elicited by a novel chimeric protein vaccine targeting GRP can suppress the proliferation of breast tumor cell EMT-6 in mice, and it may be of importance in the further exploration of the applications of other autocrine growth factor ***identified*** in human and other animal in cancer therapy.

AB . . . is an autocrine growth factor that can stimulate the growth of various cancer cells. We developed a novel protein vaccine ***HSP65*** -(GRP-10)(6) (HG6) that consists of six copies of a 10-amino acid residue epitope of GRP C-terminal fragment carried by ***mycobacterial*** 65 kDa ***HSP65*** and then immunized mice via subcutaneous injection. Strong humoral and cell-mediated immune responses were induced. High titer of anti-GRP antibodies. . . Activity of CD4+T lymphocytes, especially high levels of interferon (INF)-gamma, were developed in mice immunized with HG6 when compared with ***HSP65*** or PBS. We found that immunogene tumor therapy with a vaccine based on GRP was effective at both protective and. . . in mice, and it may be of importance in the further exploration of the applications of other autocrine growth factor ***identified*** in human and other animal in cancer therapy.

CT . . . Breast Neoplasms: PA, pathology

*Breast Neoplasms: TH, therapy

CD4-Positive T-Lymphocytes: IM, immunology

*Cancer Vaccines: AD, administration & dosage

Cell Proliferation

*** DNA Primers***

Enzyme-Linked Immunosorbent Assay

Immunization

Interferon-gamma: ME, metabolism

Lymphocyte Activation

Mice

Mice, Inbred BALB C
 Neovascularization, Pathologic
 *Peptide Fragments: . . .

CN 0 (Antibodies, Monoclonal); 0 (Cancer Vaccines); 0 (DNA ***Primers***
); 0 (Peptide Fragments); 0 (Recombinant Fusion Proteins)

L9 ANSWER 59 OF 71 MEDLINE on STN
 AN 2007352566 MEDLINE <<LOGINID::20090617>>
 DN PubMed ID: 17449684
 TI Diversity of environmental ***Mycobacterium*** isolates from
 hemodialysis water as shown by a multigene sequencing approach.

AU Gomila Margarita; Ramirez Antonio; Lalucat Jorge
 CS Area Microbiologia, Departament de Biologia, Universitat de les Illes
 Balears, Campus UIB, Crtra. Valldemosa km 7.5, Facultat de Ciències, 07122
 Palma de Mallorca, and Servei de Microbiologia, Hospital Universitari Son
 Dureta, Illes Balears, Spain.

SO Applied and environmental microbiology, (2007 Jun) Vol. 73, No. 12, pp.
 3787-97. Electronic Publication: 2007-04-20.
 Journal code: 7605801. ISSN: 0099-2240.
 Report No.: NLM-PMC1932725.

CY United States
 DT (COMPARATIVE STUDY)
 Journal; Article; (JOURNAL ARTICLE)
 (RESEARCH SUPPORT, NON-U.S. GOV'T)

LA English
 FS Priority Journals

OS GENBANK-AM421246; GENBANK-AM421247; GENBANK-AM421248; GENBANK-AM421249;
 GENBANK-AM421250; GENBANK-AM421251; GENBANK-AM421252; GENBANK-AM421253;
 GENBANK-AM421254; GENBANK-AM421255; GENBANK-AM421256; GENBANK-AM421257;
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 GENBANK-AM421262; GENBANK-AM421263; GENBANK-AM421264; GENBANK-AM421265;
 GENBANK-AM421266; GENBANK-AM421267; GENBANK-AM421268; GENBANK-AM421269;
 GENBANK-AM421270; GENBANK-AM421271; GENBANK-AM421272; GENBANK-AM421273;
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 GENBANK-AM421386; GENBANK-AM421387; GENBANK-AM421388; GENBANK-AM421389;
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 GENBANK-AM421398; GENBANK-AM421399; GENBANK-AM421400; GENBANK-AM421401;
 GENBANK-AM421402; GENBANK-AM421403; GENBANK-AM421404; GENBANK-AM421405;
 GENBANK-AM421406; GENBANK-AM421407; GENBANK-AM421408; GENBANK-AM421409;
 GENBANK-AM421410; GENBANK-AM421411; GENBANK-AM421412; GENBANK-AM421413;
 GENBANK-AM421414; GENBANK-AM421415; GENBANK-AM421416; GENBANK-AM421417;
 GENBANK-AM421418; GENBANK-AM421419; GENBANK-AM421420; GENBANK-AM421421;
 GENBANK-AM421422; GENBANK-AM421423; GENBANK-AM421424; GENBANK-AM421425;
 GENBANK-AM421426; GENBANK-AM421427; GENBANK-AM421428; GENBANK-AM421429;
 GENBANK-AM501932

EM 200803
 ED Entered STN: 15 Jun 2007
 Last Updated on STN: 7 Mar 2008
 Entered Medline: 6 Mar 2008

AB Here we used a multigene sequencing approach for the
 identification and molecular typing of environmental
 mycobacteria of the fast-growing subgroup. Strains were isolated
 from hemodialysis water and clinical samples. Eleven type strains of
 related species of the genus were also included in this study. To gain
 further insight into the diversity of the environmental
 mycobacteria, we analyzed several housekeeping genes (16S rRNA,
 ITS1, gyrB, ***hsp65***, recA, rpoB, and sodA). No individual
 phylogenetic tree allowed good discrimination of all of the species
 studied. However, a concatenated and a consensus analysis, combining the
 genes, allowed better discrimination of each strain to the species level,
 and the increase in sequence size also led to greater tree robustness.
 This approach is useful not only for the discrimination and
 identification of environmental ***mycobacteria*** but also
 for their molecular typing and studies of population genetics. Our
 results demonstrate high genetic diversity among the isolates obtained,
 which are probably new species of the genus.

TI Diversity of environmental ***Mycobacterium*** isolates from
 hemodialysis water as shown by a multigene sequencing approach.

AB Here we used a multigene sequencing approach for the
 identification and molecular typing of environmental
 mycobacteria of the fast-growing subgroup. Strains were isolated
 from hemodialysis water and clinical samples. Eleven type strains of
 related species of the genus were also included in this study. To gain
 further insight into the diversity of the environmental
 mycobacteria, we analyzed several housekeeping genes (16S rRNA,
 ITS1, gyrB, ***hsp65***, recA, rpoB, and sodA). No individual
 phylogenetic tree allowed good discrimination of all of the species
 studied. However, a concatenated. . . increase in sequence size also
 led to greater tree robustness. This approach is useful not only for the
 discrimination and ***identification*** of environmental
 mycobacteria but also for their molecular typing and studies of
 population genetics. Our results demonstrate high genetic diversity among
 the isolates. . .

CT Base Sequence
 Cluster Analysis
 *** DNA Primers: GE, genetics***

*Genes, Bacterial: GE, genetics
 *Genetic Variation
 *Hemodialysis Solutions: AN, analysis
 Molecular Sequence Data
 ****Mycobacterium: GE, genetics***
 *Phylogeny
 *Sequence Analysis, DNA: MT, methods
 Sputum: MI, microbiology
 CN 0 (DNA ***Primers***); 0 (Hemodialysis Solutions)

L9 ANSWER 60 OF 71 MEDLINE on STN
 AN 2007174460 MEDLINE <<LOGINID::20090617>>
 DN PubMed ID: 17373188
 TI ***Identification*** of novel ***hsp65*** RFLPs for
 Mycobacterium leprae.
 AU Martiniuk Frank; Tambini Marc; Rahimian Joseph; Moreira Andre; Yee Herman;
 Tchou-Wong Kam-Meng; Hanna Bruce A; Rom William N; Levis William R
 CS Department of Medicine-Pulmonary Division, New York University School of
 Medicine, New York, NY 10016, USA.. martif02@med.nyu.edu
 NC M01 RR00096 (United States NCRR NIH HHS)
 SO Journal of drugs in dermatology : JDD, (2007 Mar) Vol. 6, No. 3, pp.
 268-74.
 Journal code: 101160020. ISSN: 1545-9616.
 CY United States
 DT Journal; Article; (JOURNAL ARTICLE)
 (RESEARCH SUPPORT, N.I.H., EXTRAMURAL)
 LA English
 FS Priority Journals
 EM 200704
 ED Entered STN: 24 Mar 2007
 Last Updated on STN: 24 Apr 2007
 Entered Medline: 23 Apr 2007

AB Leprosy or Hansen's disease is a chronic infectious disease caused by an
 acid-fast bacillus, ***Mycobacterium*** leprae (M. leprae). The
 bacilli proliferate in macrophages infiltrating the skin and gain entry to
 the dermal nerves via the laminar surface of Schwann cells where they
 replicate. After entry, the Schwann cells proliferate and then die.
 Conclusive ***identification*** of M. leprae DNA in a sample can be
 obtained by polymerase chain reaction-restriction fragment length
 polymorphism (PCR-RFLP) for the heat shock 65 gene (***hsp65***).
 Molecular epidemiology will make it possible to study the global
 distributions of M. leprae, explore the relationship between
 genotypes-incidence rates, mode of transmission, and the type of disease
 (tuberculoid vs. lepromatous). We amplified DNA using PCR for the
 hsp65 gene from 24 skin lesions from patients ***diagnosed***
 with various types of leprosy. Fifteen out of 24 were positive for the
 hsp65 gene. Digestion with HaeIII-PAGE for the RFLP confirmation
 of the presence of M. leprae DNA showed the typical pattern in 5 out of 24
 and 2 novel patterns in 10 out of 24 patients. We confirmed the presence
 of M. leprae DNA by sequencing the genes for gyraseA or B and folP, which
 contained only M. leprae specific single nucleotide polymorphisms (SNPs).
 Thus, we describe novel ***hsp65*** RFLPs for M. leprae found in a
 high frequency making them ideal for future epidemiology and transmission
 studies.
 TI ***Identification*** of novel ***hsp65*** RFLPs for
 Mycobacterium leprae.
 AB Leprosy or Hansen's disease is a chronic infectious disease caused by an

acid-fast bacillus, ***Mycobacterium*** leprae (M. leprae). The bacilli proliferate in macrophages infiltrating the skin and gain entry to the dermal nerves via the laminar surface of Schwann cells where they replicate. After entry, the Schwann cells proliferate and then die. Conclusive ***identification*** of M. leprae DNA in a sample can be obtained by polymerase chain reaction-restriction fragment length polymorphism (PCR-RFLP) for the heat shock 65 gene (***hsp65***). Molecular epidemiology will make it possible to study the global distributions of M. leprae, explore the relationship between genotypes-incidence rates, mode of transmission, and the type of disease (tuberculous vs. lepromatous). We amplified DNA using PCR for the ***hsp65*** gene from 24 skin lesions from patients ***diagnosed*** with various types of leprosy. Fifteen out of 24 were positive for the ***hsp65*** gene. Digestion with HaeIII-PAGE for the RFLP confirmation of the presence of M. leprae DNA showed the typical pattern in. . . for gyraseA or B and folP, which contained only M. leprae specific single nucleotide polymorphisms (SNPs). Thus, we describe novel ***hsp65*** RFLPs for M. leprae found in a high frequency making them ideal for future epidemiology and transmission studies.

CT *Bacterial Proteins: GE, genetics
 *Chaperonins: GE, genetics
 DNA Gyrase: GE, genetics
 *** DNA Primers***
 DNA, Bacterial: CH, chemistry
 DNA, Bacterial: GE, genetics
 Electrophoresis, Polyacrylamide Gel
 Epidemiology, Molecular
 Gene Frequency
 Humans
 Leprosy: MI, microbiology
 Mycobacterium leprae: GE, genetics
 Paraffin Embedding
 Polymorphism, Restriction Fragment Length

CN 0 (Bacterial Proteins); 0 (Chaperonins); 0 (DNA ***Primers***); 0 (DNA, Bacterial); 0 (heat-shock protein 65, ***Mycobacterium***); EC 5.99.1.- (DNA Gyrase)

L9 ANSWER 61 OF 71 MEDLINE on STN
 AN 2007168555 MEDLINE <LOGINID::20090617>
 DN PubMed ID: 17369945
 TI ***Identification*** of ***mycobacteria*** of the MAIS Complex and M. tuberculosis by restriction fragment length polymorphism analysis of ***hsp65*** gene.

AU Krasnova M A; Makarova M V; Skotnikova O I; Moroz A M
 CS Moscow Municipal Scientific and Practical Center for Struggle against Tuberculosis, Moscow Department of Health.
 SO Bulletin of experimental biology and medicine, (2006 Aug) Vol. 142, No. 2, pp. 222-5.
 Journal code: 0372557. ISSN: 0007-4888.

CY United States
 DT (COMPARATIVE STUDY)
 Journal; Article; (JOURNAL ARTICLE)
 LA English; Russian
 FS Priority Journals
 EM 200704
 ED Entered STN: 20 Mar 2007
 Last Updated on STN: 28 Apr 2007

Entered Medline: 27 Apr 2007

AB Restriction fragment length polymorphism analysis of ***hsp65*** gene was performed on museum strains of ***mycobacteria*** using Hin6I restrictase. Study of restriction profiles allowed us to distinguish ***mycobacterial*** species of the MAIS complex and several strains of nontuberculous ***mycobacteria***.

TI ***Identification*** of ***mycobacteria*** of the MAIS Complex and M. tuberculosis by restriction fragment length polymorphism analysis of ***hsp65*** gene.

AB Restriction fragment length polymorphism analysis of ***hsp65*** gene was performed on museum strains of ***mycobacteria*** using Hin6I restrictase. Study of restriction profiles allowed us to distinguish ***mycobacterial*** species of the MAIS complex and several strains of nontuberculous ***mycobacteria***.

CT *Bacterial Proteins: GE, genetics
*Chaperonins: GE, genetics
*** DNA Primers***
Electrophoresis, Agar Gel
Mycobacterium: GE, genetics
Polymorphism, Restriction Fragment Length
Species Specificity

CN 0 (Bacterial Proteins); 0 (Chaperonins); 0 (DNA ***Primers***); 0 (heat-shock protein 65, ***Mycobacterium***)

L9 ANSWER 62 OF 71 MEDLINE on STN
AN 2006053996 MEDLINE <<LOGINID:20090617>>
DN PubMed ID: 16438154

TI Evaluation of polymerase chain reaction and restriction enzyme analysis for routine ***identification*** of ***mycobacteria*** : accuracy, rapidity, and cost analysis.

AU Prammananan Therdsak; Cheunoy Wattana; Na-Ubol Preeyawit; Tingtoy Nipa; Srimuang Somboon; Chaiprasert Angkana

CS Department of Microbiology, Faculty of Medicine at Siriraj Hospital, Mahidol University, Bangkok, Thailand.

SO The Southeast Asian journal of tropical medicine and public health, (2005 Sep) Vol. 36, No. 5, pp. 1252-60.
Journal code: 0266303. ISSN: 0125-1562.

CY Thailand
DT (EVALUATION STUDIES)
Journal; Article; (JOURNAL ARTICLE)
(RESEARCH SUPPORT, NON-U.S. GOV'T)

LA English
FS Priority Journals
EM 200603
ED Entered STN: 28 Jan 2006
Last Updated on STN: 1 Apr 2006
Entered Medline: 31 Mar 2006

AB Polymerase chain reaction and restriction enzyme analysis (PCR-REA) of the ***hsp65*** gene was evaluated for use as a routine ***identification*** method for ***identifying*** ***mycobacteria***. The accuracy, rapidity, and cost were assessed compared with the conventional biochemical method. Five hundred and forty-one ***mycobacterial*** clinical isolates obtained from the Department of Microbiology, Faculty of Medicine at Siriraj Hospital, Mahidol University, were submitted for PCR-REA and biochemical ***identification***. PCR-REA showed high concordant result with 100, 96.2, and 94.1% for ***identification*** of ***Mycobacterium***

tuberculosis, rapid- and slow-growing ***mycobacteria*** , respectively. Discordant results were obtained from 24 (4.4%) out of 541 isolates, consisting of 9 rapid growers (6 *M. chelonae*, 2 *M. abscessus*, and 1 *M. fortuitum*) and 15 slow growers (9 *M. scrofulaceum*, 2 *M. gordonae*, 1 *M. avium*, 1 *M. kansasii*, 1 *M. malmoeense*, and 1 *M. terrae* complex). PCR-REA demonstrated not only accurate results but was also less expensive (2.1 US dollars/sample). This method was rapid with a turn-around time of 30 hours compared with 2-4 weeks for the conventional method.

TI Evaluation of polymerase chain reaction and restriction enzyme analysis for routine ***identification*** of ***mycobacteria*** : accuracy, rapidity, and cost analysis.

AB Polymerase chain reaction and restriction enzyme analysis (PCR-REA) of the ***hsp65*** gene was evaluated for use as a routine ***identification*** method for ***identifying*** ***mycobacteria*** . The accuracy, rapidity, and cost were assessed compared with the conventional biochemical method. Five hundred and forty-one ***mycobacterial*** clinical isolates obtained from the Department of Microbiology, Faculty of Medicine at Siriraj Hospital, Mahidol University, were submitted for PCR-REA and biochemical ***identification*** . PCR-REA showed high concordant result with 100, 96.2, and 94.1% for ***identification*** of ***Mycobacterium*** tuberculosis, rapid- and slow-growing ***mycobacteria*** , respectively. Discordant results were obtained from 24 (4.4%) out of 541 isolates, consisting of 9 rapid growers (6 *M. chelonae*, . . .

CT Bacterial Proteins: IP, isolation & purification
Base Sequence
Chaperonins: IP, isolation & purification
Costs and Cost Analysis
*** DNA Primers***
DNA, Bacterial
Humans
*** Mycobacterium: CL, classification***
*** Mycobacterium: GE, genetics***
Mycobacterium: IP, isolation & purification
*Polymerase Chain Reaction
Reproducibility of Results
*Restriction Mapping
Thailand

CN 0 (Bacterial Proteins); 0 (Chaperonins); 0 (DNA ***Primers***); 0 (DNA, Bacterial); 0 (heat-shock protein 65, ***Mycobacterium***)

L9 ANSWER 63 OF 71 MEDLINE on STN
AN 2005651342 MEDLINE <<LOGINID:20090617>>
DN PubMed ID: 16332331
TI Occurrence and characterization of multiple novel genotypes of ***Mycobacterium*** immunogenum and ***Mycobacterium*** chelonae in metalworking fluids.

AU Khan Izhar U H; Selvaraju Suresh B; Yadav Jagjit S
CS Environmental Genetics and Molecular Toxicology Division, Department of Environmental Health, University of Cincinnati Medical Center, Cincinnati, OH 45267-0056, USA.

NC 1R01OH007364 (United States NIOSH CDC HHS)
SO FEMS microbiology ecology, (2005 Nov 1) Vol. 54, No. 3, pp. 329-38.
Journal code: 8901229. ISSN: 0168-6496.

CY Netherlands
DT (COMPARATIVE STUDY)
Journal; Article; (JOURNAL ARTICLE)

(RESEARCH SUPPORT, U.S. GOV'T, P.H.S.)

LA English

FS Priority Journals

EM 200606

ED Entered STN: 16 Dec 2005

Last Updated on STN: 16 Jun 2006

Entered Medline: 15 Jun 2006

AB Rapidly growing ***mycobacteria*** colonize metalworking fluids, leading to contamination of occupational environments and exposure-related respiratory illnesses in machine workers. Lately, it has been emphasized that these fluids are colonizable by a single genotype of a rapidly growing ***mycobacterium*** species, ***Mycobacterium*** immunogenum. Here, we report on the genotypic diversity of ***mycobacteria*** in these fluids, including isolation and characterization of multiple novel genotypes of two distinct species, ***Mycobacterium*** chelonae and M. immunogenum. Using agar culturing and ***Mycobacterium*** -specific PCR, 13 ***mycobacterial*** isolates were recovered from 100 geographically diverse in-use metalworking fluid samples. Based on restriction fragment length polymorphism of PCR products, DNA sequencing (***hsp65*** gene segment), and phylogenetic analysis of 16S-23S rDNA internal transcribed spacer (ITS) sequences, six isolates were ***identified*** as M. immunogenum and seven as M. chelonae; an additional isolate from metalworking fluid diluent water was ***identified*** as M. diernhoferi. Genomic DNA macro-restriction fragment pattern analysis, using pulsed-field gel electrophoresis with XbaI and SpeI restriction digestions, showed intraspecies variation among the isolates of M. immunogenum and M. chelonae. Visual and computer-assisted dendrogram analysis of the XbaI macro-restriction patterns revealed three novel genotypes of M. immunogenum and two of M. chelonae, whereas SpeI macro-restriction patterns revealed only two genotypes for each isolate. None of the ***identified*** genotypes matched the reportedly dominant one of M. immunogenum from metalworking fluids. Both ***mycobacterial*** species are prevalent in metalworking fluids and there is a considerable strain-level genetic diversity within them.

TI Occurrence and characterization of multiple novel genotypes of ***Mycobacterium*** immunogenum and ***Mycobacterium*** chelonae in metalworking fluids.

AB Rapidly growing ***mycobacteria*** colonize metalworking fluids, leading to contamination of occupational environments and exposure-related respiratory illnesses in machine workers. Lately, it has been emphasized that these fluids are colonizable by a single genotype of a rapidly growing ***mycobacterium*** species, ***Mycobacterium*** immunogenum. Here, we report on the genotypic diversity of ***mycobacteria*** in these fluids, including isolation and characterization of multiple novel genotypes of two distinct species, ***Mycobacterium*** chelonae and M. immunogenum. Using agar culturing and ***Mycobacterium*** -specific PCR, 13 ***mycobacterial*** isolates were recovered from 100 geographically diverse in-use metalworking fluid samples. Based on restriction fragment length polymorphism of PCR products, DNA sequencing (***hsp65*** gene segment), and phylogenetic analysis of 16S-23S rDNA internal transcribed spacer (ITS) sequences, six isolates were ***identified*** as M. immunogenum and seven as M. chelonae; an additional isolate from metalworking fluid diluent water was ***identified*** as M. diernhoferi. Genomic DNA macro-restriction fragment pattern analysis, using pulsed-field gel electrophoresis with XbaI and SpeI restriction

digestions, showed. . . immunogenum and two of *M. chelonae*, whereas SpeI macro-restriction patterns revealed only two genotypes for each isolate. None of the ***identified*** genotypes matched the reportedly dominant one of *M. immunogenum* from metalworking fluids. Both ***mycobacterial*** species are prevalent in metalworking fluids and there is a considerable strain-level genetic diversity within them.

CT Bacterial Proteins: GE, genetics
Base Sequence
Chaperonins: GE, genetics
Cluster Analysis
*** DNA Primers***
DNA, Ribosomal: GE, genetics
Electrophoresis, Gel, Pulsed-Field
Genotype
*Metallurgy
Molecular Sequence Data
Mycobacterium: GE, genetics
*Occupational Exposure
*Phylogeny
Polymorphism, Restriction Fragment Length
Sequence Analysis, DNA
Species Specificity
*Water Microbiology

CN 0 (Bacterial Proteins); 0 (Chaperonins); 0 (DNA ***Primers***); 0 (DNA, Ribosomal); 0 (heat-shock protein 65, ***Mycobacterium***)

L9 ANSWER 64 OF 71 MEDLINE on STN
AN 2001092058 MEDLINE <LOGINID:20090617>
DN PubMed ID: 11090265
TI Description of a novel ***Mycobacterium*** simiae allelic variant isolated from Caribbean AIDS patients by PCR-restriction enzyme analysis and sequencing of ***hsp65*** gene.
AU Legrand E; Goh K S; Sola C; Rastogi N
CS Unite de la Tuberculose et des Mycobacteries, Institut Pasteur, BP 484, F-97165 Pointe a Pitre-Cedex, Guadeloupe.
SO Molecular and cellular probes, (2000 Dec) Vol. 14, No. 6, pp. 355-63. Journal code: 8709751. ISSN: 0890-8508.
CY ENGLAND: United Kingdom
DT Journal; Article; (JOURNAL ARTICLE)
(RESEARCH SUPPORT, NON-U.S. GOV'T)
LA English
FS Priority Journals
EM 200101
ED Entered STN: 22 Mar 2001
Last Updated on STN: 22 Mar 2001
Entered Medline: 25 Jan 2001

AB A sudden upsurge in the isolation of ***Mycobacterium*** simiae from terminally ill AIDS patients was recently reported on the Caribbean island of Guadeloupe. ***Identification*** of these *M. simiae* isolates was achieved using biochemical tests and further confirmed by PCR-restriction analysis (PRA) of a 439-bp fragment of ***hsp65***. A novel PRA profile III (three Bst EII fragments of 240/125/80 bp and four Hae III fragments of 145/125/40/25 bp) was observed in four blood isolates from two patients. The 16 S rRNA gene sequencing of the hypervariable A region confirmed that all the pattern III isolates were indeed *M. simiae* species, and the ***hsp65*** sequencing confirmed the existence of a new ***hsp65*** allele in these caribbean isolates. A ***hsp65***

sequence-based phylogenetic tree was also created for 39 species including *M. simiae* and related ***mycobacterial*** species as well as other rapid and slow growing ***mycobacteria***, and may serve as an useful tool for ***identification*** of ***mycobacteria*** to species level.

Copyright 2000 Academic Press.

TI Description of a novel ***Mycobacterium*** *simiae* allelic variant isolated from Caribbean AIDS patients by PCR-restriction enzyme analysis and sequencing of ***hsp65*** gene.

AB A sudden upsurge in the isolation of ***Mycobacterium*** *simiae* from terminally ill AIDS patients was recently reported on the Caribbean island of Guadeloupe. ***Identification*** of these *M. simiae* isolates was achieved using biochemical tests and further confirmed by PCR-restriction analysis (PRA) of a 439-bp fragment of ***hsp65***. A novel PRA profile III (three Bst EII fragments of 240/125/80 bp and four Hae III fragments of 145/125/40/25 bp). . . sequencing of the hypervariable A region confirmed that all the pattern III isolates were indeed *M. simiae* species, and the ***hsp65*** sequencing confirmed the existence of a new ***hsp65*** allele in these caribbean isolates. A ***hsp65*** sequence-based phylogenetic tree was also created for 39 species including *M. simiae* and related ***mycobacterial*** species as well as other rapid and slow growing ***mycobacteria***, and may serve as an useful tool for ***identification*** of ***mycobacteria*** to species level.

Copyright 2000 Academic Press.

CT . . .

Immunodeficiency Syndrome: MI, microbiology

Adult

Aged

Alleles

*Bacterial Proteins

Base Sequence

*Chaperonins: GE, genetics

DNA: AN, analysis

DNA: BL, blood

*** DNA Primers: CH, chemistry***

*DNA, Bacterial: AN, analysis

DNA, Ribosomal: GE, genetics

*Genetic Variation

Genome, Bacterial

Guadeloupe: EP, epidemiology

Humans

Middle Aged

Molecular Sequence Data

Mycobacterium: IP, isolation & purification

*** Mycobacterium Infections: EP, epidemiology***

*** Mycobacterium Infections: GE, genetics***

Mycobacterium Infections: MI, microbiology

Phylogeny

*Polymerase Chain Reaction: MT, methods

*Restriction Mapping: MT, methods

Sequence Alignment

Sequence Homology, Nucleic Acid

CN 0 (Bacterial Proteins); 0 (Chaperonins); 0 (DNA ***Primers***); 0 (DNA, Bacterial); 0 (DNA, Ribosomal); 0 (heat-shock protein 65, ***Mycobacterium***)

L9 ANSWER 65 OF 71 MEDLINE on STN
 AN 1998010213 MEDLINE <<LOGINID::20090617>>
 DN PubMed ID: 9350730
 TI Molecular characterization of ***Mycobacterium*** avium complex
 isolates giving discordant results in AccuProbe tests by PCR-restriction
 enzyme analysis, 16S rRNA gene sequencing, and DT1-DT6 PCR.
 AU Devallois A; Picardeau M; Paramasivan C N; Vincent V; Rastogi N
 CS Unite de la Tuberculose et des Mycobacteries, Institut Pasteur,
 Pointe-a-Pitre, Guadeloupe, French West Indies.
 SO Journal of clinical microbiology, (1997 Nov) Vol. 35, No. 11, pp. 2767-72.
 Journal code: 7505564. ISSN: 0095-1137.
 Report No.: NLM-PMC230058.
 CY United States
 DT (COMPARATIVE STUDY)
 Journal; Article; (JOURNAL ARTICLE)
 (RESEARCH SUPPORT, NON-U.S. GOV'T)
 LA English
 FS Priority Journals
 EM 199802
 ED Entered STN: 17 Feb 1998
 Last Updated on STN: 17 Feb 1998
 Entered Medline: 3 Feb 1998
 AB Based on cultural and biochemical tests, a total of 84 strains (72
 clinical and 12 environmental isolates from the Caribbean Isles, Europe,
 and the Indian subcontinent) were ***identified*** as members of the
 Mycobacterium avium complex (MAC). They were further
 characterized with MAC, M. avium, and M. intracellulare probes of the
 AccuProbe system, and this was followed by selective amplification of DT6
 and DT1 sequences. Seventy isolates gave concordant results; 63 were
 identified as M. avium, 5 were ***identified*** as M.
 intracellulare, and 24 remained untypeable by both methods. Fourteen
 isolates gave discrepant results, as they were DT1 positive but gave
 negative results by the M. intracellulare AccuProbe test. Consequently, a
 detailed molecular analysis of all DT1-positive isolates (14 discrepant
 strains plus 5 M. intracellulare strains) was performed by PCR-restriction
 analysis (PRA) of the ***hsp65*** gene and 16S rRNA gene sequencing.
 The results confirmed the reported heterogeneity of M. intracellulare, as
 only 6 of 19 isolates (32%) gave PRA results compatible with published M.
 intracellulare profiles while the rest of the isolates were grouped in
 four previously unpublished profiles. 16S rRNA gene sequencing showed that
 only 8 of 19 isolates (42%) were related to M. intracellulare INGMT 90247
 (EMBL accession no. X88917), the rest being related to MCR019 (EMBL
 accession no. X93030) and MIWGTMR10 (EMBL accession no. X88915). In
 conclusion, we have characterized a significant number of MAC isolates
 which were not ***identified*** by the AccuProbe test, PRA, or 16S
 rRNA sequencing. However, all of them were ***identifiable*** by
 DT1-DT6 PCR (they were DT6 negative and DT1 positive) and could be
 tentatively ***identified*** as M. intracellulare based on previously
 published observations. It is noteworthy that the majority of such
 isolates (14 of 19) were from the Indian subcontinent, with 12 of 14 being
 environmental isolates. Our study confirms the marked heterogeneity of M.
 intracellulare isolates and shows the utility of in-house DT1 PCR to
 detect this group of isolates, which would otherwise have been missed by
 the AccuProbe system in a routine clinical microbiology laboratory.
 TI Molecular characterization of ***Mycobacterium*** avium complex
 isolates giving discordant results in AccuProbe tests by PCR-restriction
 enzyme analysis, 16S rRNA gene sequencing, and DT1-DT6 PCR.. . .

AB . . . total of 84 strains (72 clinical and 12 environmental isolates from the Caribbean Isles, Europe, and the Indian subcontinent) were ***identified*** as members of the ***Mycobacterium*** avium complex

(MAC). They were further characterized with MAC, M. avium, and M. intracellulare probes of the AccuProbe system, and this was followed by selective amplification of DT6 and DT1 sequences. Seventy isolates gave concordant results; 63 were ***identified*** as M. avium, 5 were ***identified*** as M. intracellulare, and 24 remained untypeable by both methods. Fourteen isolates gave discrepant results, as they were DT1 positive. . . of all DT1-positive isolates (14 discrepant strains plus 5 M. intracellulare strains) was performed by PCR-restriction analysis (PRA) of the ***hsp65*** gene and 16S rRNA gene sequencing. The results confirmed the reported heterogeneity of M. intracellulare, as only 6 of 19. . . and MIWGTR10 (EMBL accession no. X88915). In conclusion, we have characterized a significant number of MAC isolates which were not ***identified*** by the AccuProbe test, PRA, or 16S rRNA sequencing. However, all of them were ***identifiable*** by DT1-DT6 PCR (they were DT6 negative and DT1 positive) and could be tentatively ***identified*** as M. intracellulare based on previously published observations. It is noteworthy that the majority of such isolates (14 of 19). . .

CT Base Sequence
 *** DNA Primers***
 DNA, Bacterial: GE, genetics
 *DNA, Ribosomal: GE, genetics
 Europe
 Genetic Variation
 Guadeloupe
 Humans
 India
 Molecular Sequence Data
 *** Mycobacterium avium Complex: CL, classification***
 Mycobacterium avium Complex: GE, genetics
 Mycobacterium avium Complex: IP, isolation & purification
 Mycobacterium avium-intracellulare Infection: DI, diagnosis
 *Polymerase Chain Reaction: MT, methods
 *RNA, Ribosomal, 16S: GE, genetics
 *** Reagent Kits, Diagnostic***
 Sequence Alignment
 Sequence Homology, Nucleic Acid

CN 0 (DNA ***Primers***); 0 (DNA, Bacterial); 0 (DNA, Ribosomal); 0 (RNA, Ribosomal, 16S); 0 (Reagent Kits, ***Diagnostic***)

L9 ANSWER 66 OF 71 MEDLINE on STN
 AN 1997424502 MEDLINE <LOGINID:20090617>
 DN PubMed ID: 9278615
 TI Routine rapid ***Mycobacterium*** species assignment based on species-specific allelic variation in the 65-kilodalton heat shock protein gene (***hsp65***).

AU Pai S; Esen N; Pan X; Musser J M
 CS Clinical Microbiology Laboratory, Methodist Hospital Houston, Tex, USA.
 NC DA-09238 (United States NIDA NIH HHS)
 SO Archives of pathology & laboratory medicine, (1997 Aug) Vol. 121, No. 8, pp. 859-64.
 Journal code: 7607091. ISSN: 0003-9985.
 CY United States

DT Journal; Article; (JOURNAL ARTICLE)
(RESEARCH SUPPORT, U.S. GOV'T, P.H.S.)

LA English

FS Abridged Index Medicus Journals; Priority Journals

EM 199709

ED Entered STN: 8 Oct 1997

Last Updated on STN: 3 Mar 2000

Entered Medline: 19 Sep 1997

AB OBJECTIVE: To assess the utility of automated DNA sequencing strategies for ***Mycobacterium*** species assignment and surrogate rifampin susceptibility testing of ***Mycobacterium*** tuberculosis complex isolates in a hospital-based clinical microbiology laboratory. DESIGN: Consecutive patient specimens (n = 161) cultured in BACTEC 12B medium (growth index of 50 or greater) or on solid media (Lowenstein-Jensen) were analyzed. A 360-bp segment of a gene (***hsp65***) encoding a 65-kd heat shock protein was sequenced to ***identify*** species-specific allelic polymorphism. ***Identification*** of sequence variation in the rpoB gene encoding the beta subunit of RNA polymerase was used as a surrogate method to assess rifampin susceptibility in M tuberculosis complex isolates. RESULTS: The automated DNA sequencing strategies rapidly ***identified*** virtually all ***mycobacteria*** (158 [98%] of 161) to the species level and unambiguously characterized the region of rpoB that contains mutations responsible for rifampin resistance in M tuberculosis strains. With few exceptions, DNA sequence-based species assignment data agreed with ***diagnostic*** information obtained by conventional methods. All discrepancies were due to ambiguous biochemical test data or interpretation. The rifampin susceptibility phenotype was correctly predicted for all strains by rpoB sequencing. CONCLUSIONS: Rapid ***mycobacterial*** species assignment based on ***hsp65*** sequencing can be routinely performed in a hospital ***diagnostic*** microbiology laboratory setting. The method is especially useful for ***identification*** of fastidious organisms, such as ***Mycobacterium*** genavense. Sequencing of the rifampin-resistance-determining region of rpoB provides a convenient surrogate strategy for predicting rifampin susceptibility in M tuberculosis complex isolates.

TI Routine rapid ***Mycobacterium*** species assignment based on species-specific allelic variation in the 65-kilodalton heat shock protein gene (***hsp65***).

AB OBJECTIVE: To assess the utility of automated DNA sequencing strategies for ***Mycobacterium*** species assignment and surrogate rifampin susceptibility testing of ***Mycobacterium*** tuberculosis complex isolates in a hospital-based clinical microbiology laboratory. DESIGN: Consecutive patient specimens (n = 161) cultured in BACTEC 12B. . . medium (growth index of 50 or greater) or on solid media (Lowenstein-Jensen) were analyzed. A 360-bp segment of a gene (***hsp65***) encoding a 65-kd heat shock protein was sequenced to ***identify*** species-specific allelic polymorphism. ***Identification*** of sequence variation in the rpoB gene encoding

the

beta subunit of RNA polymerase was used as a surrogate method to assess rifampin susceptibility in M tuberculosis complex isolates. RESULTS: The automated DNA sequencing strategies rapidly ***identified*** virtually all ***mycobacteria*** (158 [98%] of 161) to the species level and unambiguously characterized the region of rpoB that contains mutations responsible for rifampin resistance in M tuberculosis strains. With few exceptions, DNA sequence-based species assignment data agreed with

diagnostic information obtained by conventional methods. All discrepancies were due to ambiguous biochemical test data or interpretation. The rifampin susceptibility phenotype was correctly predicted for all strains by rpoB sequencing. CONCLUSIONS: Rapid ***mycobacterial*** species assignment based on ***hsp65*** sequencing can be routinely performed in a hospital ***diagnostic*** microbiology laboratory setting. The method is especially useful for ***identification*** of fastidious organisms, such as ***Mycobacterium*** genavense. Sequencing of the rifampin-resistance-determining region of rpoB provides a convenient surrogate strategy for predicting rifampin susceptibility in M tuberculosis. . . .

CT Alleles
 *Bacterial Proteins: GE, genetics
 Bacterial Typing Techniques
 *Chaperonins: GE, genetics
 *** DNA Primers: CH, chemistry***
 *DNA, Bacterial: AN, analysis
 DNA-Directed RNA Polymerases: GE, genetics
 Humans
 Microbial Sensitivity Tests
 Mycobacterium: CL, classification
 *** Mycobacterium: GE, genetics***
 *** Mycobacterium: IP, isolation & purification***
 *** Mycobacterium tuberculosis: DE, drug effects***
 *** Mycobacterium tuberculosis: GE, genetics***
 *** Mycobacterium tuberculosis: IP, isolation & purification***
 Polymerase Chain Reaction
 Rifampin: PD, pharmacology
 Sequence Analysis, DNA: MT, methods

CN 0 (Bacterial Proteins); 0 (Chaperonins); 0 (DNA ***Primers***); 0 (DNA, Bacterial); 0 (heat-shock protein 65, ***Mycobacterium***); EC 2.7.7.6 (DNA-Directed RNA Polymerases); EC 2.7.7.6 (RNA polymerase beta subunit)

L9 ANSWER 67 OF 71 MEDLINE on STN
 AN 1997256941 MEDLINE <<LOGINID::20090617>>
 DN PubMed ID: 9103645
 TI ***Mycobacterium*** mageritense sp. nov.
 AU Domenech P; Jimenez M S; Menendez M C; Bull T J; Samper S; Manrique A; Garcia M J
 CS Departamento de Medicina Preventiva, Facultad de Medicina, Universidad Autonoma de Madrid, Spain.
 SO International journal of systematic bacteriology, (1997 Apr) Vol. 47, No. 2, pp. 535-40.
 Journal code: 0042143. ISSN: 0020-7713.
 CY United States
 DI (COMPARATIVE STUDY)
 Journal; Article; (JOURNAL ARTICLE)
 (RESEARCH SUPPORT, NON-U.S. GOV'T)

LA English
 FS Priority Journals
 OS GENBANK-M29558; GENBANK-M29566; GENBANK-M29567; GENBANK-M59056; GENBANK-U77305; GENBANK-U86083; GENBANK-U86084; GENBANK-U86085; GENBANK-U86086; GENBANK-U86087; GENBANK-U86088; GENBANK-U86089; GENBANK-X52861; GENBANK-X52921; GENBANK-X52922; GENBANK-X52933; GENBANK-X55599; GENBANK-X58890; GENBANK-X65528; GENBANK-X65529;

GENBANK-X80771; GENBANK-X81385; GENBANK-X81392; GENBANK-X82235;
 GENBANK-X82236; GENBANK-X86082; GENBANK-X99838; GENBANK-Z48211;
 GENBANK-Z48214; GENBANK-Z48216; +
 EM 199706
 ED Entered STN: 12 Jun 1997
 Last Updated on STN: 12 Jun 1997
 Entered Medline: 3 Jun 1997
 AB Strains of a new species of rapidly growing, nonphotochromogenic
 Mycobacteria, ***Mycobacterium*** mageritense, were isolated
 from human sputum. The growth characteristics, acid fastness, and mycolic
 acids of the isolates were consistent with those of ***Mycobacterium***
 species. The isolates were ***identified*** as members of a new
 species by performing a biochemical analysis and DNA-DNA hybridization
 experiments, and by comparing the sequences of several conserved genes,
 such as the 16S rRNA, ***hsp65***, and sodA genes. A phylogenetic
 analysis in which 16S rRNA and sodA sequences were used ***identified***
 M. mageritense as a novel distinct species and placed M. mageritense
 between members of the ***Mycobacterium*** fortuitum complex and the
 thermotolerant rapidly growing group. Our results demonstrate that the
 taxonomic value of sodA sequence analysis in the genus
 Mycobacterium is similar to the well-established value of 16S
 rRNA
 sequence analysis.
 TI ***Mycobacterium*** mageritense sp. nov.
 AB Strains of a new species of rapidly growing, nonphotochromogenic
 Mycobacteria, ***Mycobacterium*** mageritense, were isolated
 from human sputum. The growth characteristics, acid fastness, and mycolic
 acids of the isolates were consistent with those of ***Mycobacterium***
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 such as the 16S rRNA, ***hsp65***, and sodA genes. A phylogenetic
 analysis in which 16S rRNA and sodA sequences were used ***identified***
 M. mageritense as a novel distinct species and placed M. mageritense
 between members of the ***Mycobacterium*** fortuitum complex and the
 thermotolerant rapidly growing group. Our results demonstrate that the
 taxonomic value of sodA sequence analysis in the genus
 Mycobacterium is similar to the well-established value of 16S
 rRNA
 sequence analysis.
 CT Bacterial Proteins: GE, genetics
 Base Sequence
 *** DNA Primers: GE, genetics***
 DNA, Bacterial: GE, genetics
 Genes, Bacterial
 Humans
 Molecular Sequence Data
 Mycobacterium: CL, classification
 Mycobacterium: GE, genetics
 Mycobacterium: IP, isolation & purification
 Phylogeny
 Polymerase Chain Reaction
 Polymorphism, Restriction Fragment Length
 RNA, Bacterial: GE, genetics
 RNA, Ribosomal, 16S: . . .
 CN 0 (Bacterial Proteins); 0 (DNA ***Primers***); 0 (DNA, Bacterial); 0
 (RNA, Bacterial); 0 (RNA, Ribosomal, 16S); 0 (SodA protein, Bacteria); EC

1.15.1.1 (Superoxide Dismutase)

L9 ANSWER 68 OF 71 MEDLINE on STN
 AN 1997256926 MEDLINE <<LOGINID::20090617>>
 DN PubMed ID: 9103630
 TI Subspecific differentiation of ***Mycobacterium*** avium complex strains by automated sequencing of a region of the gene (***hsp65***) encoding a 65-kilodalton heat shock protein.
 AU Swanson D S; Kapur V; Stockbauer K; Pan X; Frothingham R; Musser J M
 CS Department of Pediatrics, Baylor College of Medicine, Houston, Texas 77030, USA.
 NC AI07392 (United States NIAID NIH HHS)
 AI37004 (United States NIAID NIH HHS)
 DA09238 (United States NIDA NIH HHS)
 +
 SO International journal of systematic bacteriology, (1997 Apr) Vol. 47, No. 2, pp. 414-9.
 Journal code: 0042143. ISSN: 0020-7713.
 CY United States
 DT (COMPARATIVE STUDY)
 Journal; Article; (JOURNAL ARTICLE)
 (RESEARCH SUPPORT, NON-U.S. GOV'T)
 (RESEARCH SUPPORT, U.S. GOV'T, NON-P.H.S.)
 (RESEARCH SUPPORT, U.S. GOV'T, P.H.S.)
 LA English
 FS Priority Journals
 OS GENBANK-U85631; GENBANK-U85632; GENBANK-U85633; GENBANK-U85634;
 GENBANK-U85635; GENBANK-U85636; GENBANK-U85637; GENBANK-U85638;
 GENBANK-U85639; GENBANK-U85640; GENBANK-U85641
 EM 199706
 ED Entered STN: 12 Jun 1997
 Last Updated on STN: 29 Jan 1999
 Entered Medline: 3 Jun 1997
 AB To develop a strategy for rapid species assignment and strain differentiation of ***Mycobacterium*** avium complex (MAC) organisms, the sequence of a 360-bp region of the gene (***hsp65***) encoding a 65-kDa heat shock protein was determined for 56 isolates, including 21 patient isolates and 35 reference strains. Eleven ***hsp65*** alleles were ***identified***, and there was no sharing of alleles between strains classified as M. avium and ***Mycobacterium*** intracellular based on serovar and species-specific DNA hybridization probes. Phylogenetic analysis showed that 30 strains had one of two ***hsp65*** alleles which were found in known M. avium organisms, 23 strains had one of six alleles allied with known M. intracellular organisms, and three MAC isolates had one of three ***hsp65*** alleles that differed substantially from the consensus M. avium and M. intracellular ***hsp65*** sequences. Estimates of strain relationships based on the sequences of ***hsp65*** and the 16S-23S ribosomal DNA internal transcribed spacer were similar. Automated DNA sequencing of a 360-bp region of the ***hsp65*** gene from MAC organisms provides a rapid and unambiguous marker system for strain differentiation and permits specific assignment of these acid-fast organisms for ***diagnostic*** purposes.
 TI Subspecific differentiation of ***Mycobacterium*** avium complex strains by automated sequencing of a region of the gene (***hsp65***) encoding a 65-kilodalton heat shock protein.
 AB To develop a strategy for rapid species assignment and strain differentiation of ***Mycobacterium*** avium complex (MAC) organisms,

the sequence of a 360-bp region of the gene (***hsp65***) encoding a 65-kDa heat shock protein was determined for 56 isolates, including 21 patient isolates and 35 reference strains. Eleven ***hsp65*** alleles were ***identified*** , and there was no sharing of alleles between strains classified as *M. avium* and ***Mycobacterium*** intracellular based on serovar and species-specific DNA hybridization probes. Phylogenetic analysis showed that 30 strains had one of two ***hsp65*** alleles which were found in known *M. avium* organisms, 23 strains had one of six alleles allied with known *M. intracellulare* organisms, and three MAC isolates had one of three ***hsp65*** alleles that differed substantially from the consensus *M. avium* and *M. intracellulare* ***hsp65*** sequences. Estimates of strain relationships based on the sequences of ***hsp65*** and the 16S-23S ribosomal DNA internal transcribed spacer were similar. Automated DNA sequencing of a 360-bp region of the ***hsp65*** gene from MAC organisms provides a rapid and unambiguous marker system for strain differentiation and permits specific assignment of these acid-fast organisms for ***diagnostic*** purposes.

CT Alleles
 *Bacterial Proteins
 Base Sequence
 *Chaperonins: GE, genetics
 *** DNA Primers: GE, genetics***
 DNA, Bacterial: GE, genetics
 DNA, Ribosomal: GE, genetics
 *Genes, Bacterial
 Humans
 Molecular Sequence Data
 ****Mycobacterium avium Complex: CL, classification***
 ****Mycobacterium avium Complex: GE, genetics***
 *** Mycobacterium avium Complex: IF, isolation & purification***
 Phylogeny
 Polymorphism, Genetic
 RNA, Bacterial: GE, genetics
 RNA, Ribosomal, 16S: GE, genetics
 RNA, . . .

CN 0 (Bacterial Proteins); 0 (Chaperonins); 0 (DNA ***Primers***); 0 (DNA, Bacterial); 0 (DNA, Ribosomal); 0 (RNA, Bacterial); 0 (RNA, Ribosomal, 16S); 0 (RNA, Ribosomal, 23S); 0 (heat-shock protein 65, ***Mycobacterium***)

L9 ANSWER 69 OF 71 SCISEARCH COPYRIGHT (c) 2009 The Thomson Corporation on STN

AN 2005:974796 SCISEARCH <<LOGINID:20090617>>

GA The Genuine Article (R) Number: 966LD

TI Method for rapid ***identification*** and differentiation of the species of the ***Mycobacterium*** chelonae complex based on 16S-23S rRNA gene internal transcribed Spacer PCR-restriction analysis

AU Yadav J S (Reprint)

CS Univ Cincinnati, Med Ctr, Dept Environm Hlth, Environm Genet & Mol Toxicol Div, Cincinnati, OH 45267 USA (Reprint)

AU Khan I U H; Selvaraju S B

CS E-mail: Jagjit.Yadav@uc.edu

CYA USA

SO JOURNAL OF CLINICAL MICROBIOLOGY, (SEP 2005) Vol. 43, No. 9, pp. 4466-4472.
 ISSN: 0095-1137.

PB AMER SOC MICROBIOLOGY, 1752 N ST NW, WASHINGTON, DC 20036-2904 USA.

DT Article; Journal
LA English

REC Reference Count: 26
ED Entered STN: 6 Oct 2005

Last Updated on STN: 6 Oct 2005

ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

AB Members of the ***Mycobacterium*** chelonae complex (MCC), including *M. immunogenum*, *M. chelonae*, and *M. abscessus*, have been associated with nosocomial infections and occupational hypersensitivity pneumonitis due to metalworking fluid (MWF) exposures. In order to minimize these health hazards, an effective and rapid assay for detection of MCC species and differentiation of MCC species from other species of rapidly growing ***mycobacteria*** (RGM) and from one another is warranted. Here we report such a method, based on the variable 16S-23S rRNA gene internal transcribed spacer (ITS) region. ***Mycobacterium*** genus-specific ***primers*** derived from highly conserved sequences in the ITS region and the flanking 16S rRNA gene were used. Specificity of the ***primers*** was verified using the MCC member species, 11 non-MCC RGM species, 3 slow-growing ***mycobacterial*** (SGM) species (two strains each), and 19 field isolates, including 18 MCC isolates (from in-use MWF) and one non-MCC isolate (from reverse osmosis water). The ITS amplicon size of *M. immunogenum* varied from those of *M. chelonae* and *M. abscessus*. Sequencing of the similar to 250-bp-long ITS amplicons of the three MCC member species showed differences in 24 to 34 bases, thereby yielding variable deduced restriction maps. ITS PCR-restriction analysis using the *in silico*-selected restriction enzyme MaeII or HphI differentiated the three MCC members from one another and from other RGM and SGM species without sequencing. The enzyme MaeII discriminated all three member species; however, HphI could only differentiate *M. immunogenum* from *M. chelonae* and *M. abscessus*. Use of an optimized rapid DNA template preparation step based on direct cell lysis in the PCR tube added to the simplicity and adaptability of the developed assay.

TI Method for rapid ***identification*** and differentiation of the species of the ***Mycobacterium*** chelonae complex based on 16S-23S rRNA gene internal transcribed Spacer PCR-restriction analysis

AB Members of the ***Mycobacterium*** chelonae complex (MCC), including *M. immunogenum*, *M. chelonae*, and *M. abscessus*, have been associated with nosocomial infections and occupational hypersensitivity. . . effective and rapid assay for detection of MCC species and differentiation of MCC species from other species of rapidly growing ***mycobacteria*** (RGM) and from one another is warranted. Here we report such a method, based on the variable 16S-23S rRNA gene internal transcribed spacer (ITS) region. ***Mycobacterium*** genus-specific ***primers*** derived from highly conserved sequences in the ITS region and the flanking 16S rRNA gene were used. Specificity of the ***primers*** was verified using the MCC member species, 11 non-MCC RGM species, 3 slow-growing ***mycobacterial*** (SGM) species (two strains each), and 19 field isolates, including 18 MCC isolates (from in-use MWF) and one non-MCC isolate. . .

STP KeyWords Plus (R): LENGTH POLYMORPHISM ANALYSIS; HYPERSENSITIVITY PNEUMONITIS; ***HSP65*** GENE; FORTUITUM; ABSCESSUS; SEQUENCES; STRAINS; CRITERIA; MACHINE; ***PRIMERS***

L9 ANSWER 70 OF 71 SCISEARCH COPYRIGHT (c) 2009 The Thomson Corporation on STN

AN 2003:336370 SCISEARCH <<LOGINID:20090617>>

GA The Genuine Article (R) Number: 666LZ

TI PCR-based method to differentiate the subspecies of the
 Mycobacterium tuberculosis complex on the basis of genomic deletions

AU Ho J L (Reprint)

CS Cornell Univ, Joan & Sanford I Weill Med Coll, Dept Med, Div Int Med & Infect Dis, Room A-421, 525 E 68th St, New York, NY 10021 USA (Reprint)

AU Huard R C; Lazzarini L C D; Butler W R; van Soolingen D

CS Cornell Univ, Joan & Sanford I Weill Med Coll, Dept Med, Div Int Med & Infect Dis, New York, NY 10021 USA; Cornell Univ, Grad Sch Med Sci, New York, NY 10021 USA; Ctr Dis Control & Prevent, Div AIDS STD & TB Lab Res, Natl Ctr Infect Dis, Atlanta, GA USA; Natl Inst Publ Hlth & Environm, NL-3720 BA Bilthoven, Netherlands

CYA USA; Netherlands

SO JOURNAL OF CLINICAL MICROBIOLOGY, (APR 2003) Vol. 41, No. 4, pp. 1637-1650.
 ISSN: 0095-1137.

PB AMER SOC MICROBIOLOGY, 1752 N ST NW, WASHINGTON, DC 20036-2904 USA.

DT Article; Journal

LA English

REC Reference Count: 45

ED Entered STN: 2 May 2003
 Last Updated on STN: 2 May 2003

ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

AB The classical ***Mycobacterium*** tuberculosis complex (MtbC) subspecies include ***Mycobacterium*** tuberculosis, ***Mycobacterium*** africanum (subtypes I and II), ***Mycobacterium*** bovis (along with the attenuated *M. bovis* bacillus Calmette-Guerin [BCG]), and ***Mycobacterium*** microti; increasingly recognized MtbC groupings include ***Mycobacterium*** bovis subsp. caprae and " ***Mycobacterium*** tuberculosis subsp. canettii" Previous investigations have documented each MtbC subspecies as a source of animal and/or human tuberculosis. However, study of these organisms is hindered by the lack of a single protocol that quickly and easily differentiates all of the MtbC groupings. Towards this end we have developed a rapid, simple, and reliable PCR-based MtbC typing method that makes use of MtbC chromosomal region-of-difference deletion loci. Here, seven ***primer*** pairs (which amplify within the loci 16S rRNA, Rv0577, IS1561', Rv1510, Rv1970, Rv3877/8, and Rv3120) were run in separate but simultaneous reactions. Each ***primer*** pair either specifically amplified a DNA fragment of a unique size or failed, depending upon the source ***mycobacterial*** DNA. The pattern of amplification products from all of the reactions, visualized by agarose gel electrophoresis, allowed immediate ***identification*** either as MtbC composed of *M. tuberculosis* (or *M. africanum* subtype II), *M. africanum* subtype I, *M. bovis*, *M. bovis* BCG, *M. caprae*, *M. micron*, or "*M. canettii*" or as a ***Mycobacterium*** other than MtbC (MOTT). This MtbC PCR typing panel provides an advanced approach to determine the subspecies of MtbC isolates and to differentiate them from clinically important MOTT species. It has proven beneficial in the management of ***Mycobacterium*** collections and may be applied for practical clinical and epidemiological use.

TI PCR-based method to differentiate the subspecies of the
 Mycobacterium tuberculosis complex on the basis of genomic deletions

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STP KeyWords Plus (R): FRAGMENT LENGTH POLYMORPHISM; GENETIC-MARKERS; BOVIS
 STRAINS; WEST-AFRICA; ***HSP65*** GENE; ***IDENTIFICATION*** ;
 SEQUENCE; EPIDEMIOLOGY; INFECTION; ***DIAGNOSIS***

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GA The Genuine Article (R) Number: 190CL

TI Solid-phase sequence scanning for drug resistance detection in
 tuberculosis

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AB DNA chip arrays hold considerable promise for ***diagnostic***
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mutation detection by ***primer*** -extension-based sequence scanning of the rpoB gene of M. tuberculosis are presented. Rifampin resistant clinical isolates were ***identified*** in as little as 1 h post PCR amplification with visual results detection. (C) 1999 Academic Press.

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ST Author Keywords: ***Mycobacterium*** tuberculosis; drug resistance; DNA arrays; GBA; solid-phase; ***primer*** extension

STP KeyWords Plus (R): HEAT-SHOCK-PROTEIN; CATALASE-PEROXIDASE GENE; ***MYCOBACTERIUM*** -TUBERCULOSIS; SUBSPECIFIC DIFFERENTIATION; ISONIAZID

RESISTANCE; BIT ANALYSIS; ***HSP65*** ; ***IDENTIFICATION*** ; SENSITIVITY; ETHAMBUTOL